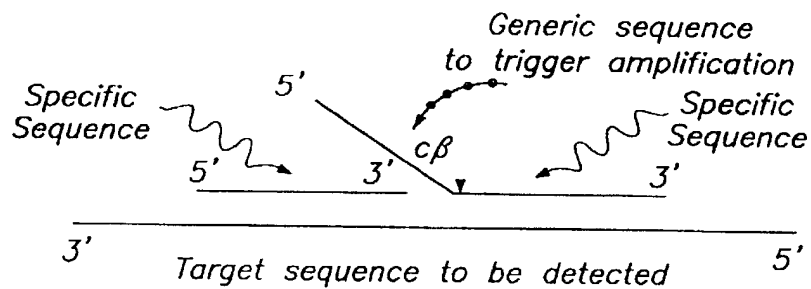
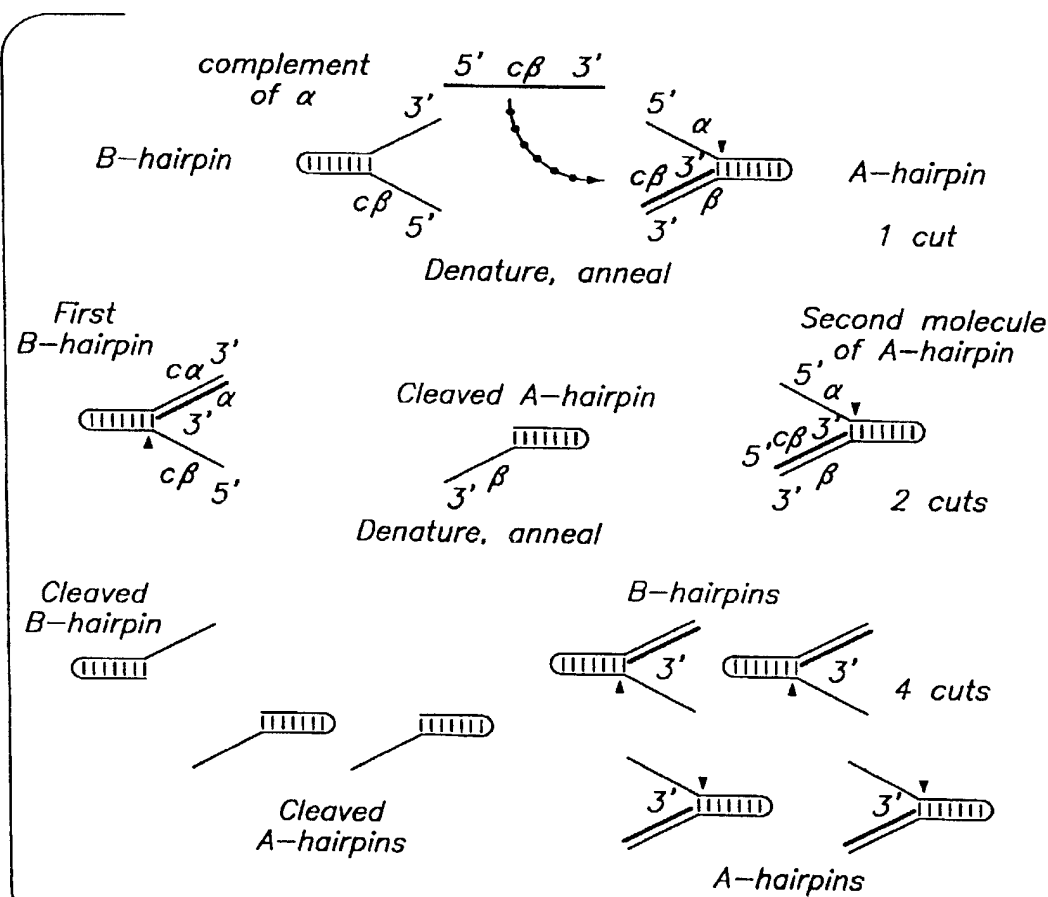


FIG. 1A



**FIG. 1B** PART ONE: TRIGGER REACTION



**FIG. 1C** PART TWO: DETECTION REACTION

MAJORITY	[SEQ ID NO:7]	ATGXXGGGGATGCTTCCCTCTTTGAGCGCCAAAGGCGGGGTCTCTCTGGTGGACGGCCACACCTGGCGT
DNAPTAO	[SEQ ID NO:1]	...AG..G.....G.....G.....
DNAPTFL	[SEQ ID NO:2]	.....C..G.....
DNAPTTH	[SEQ ID NO:3]	...GA.....G.....A.....
MAJORITY		ACCGCACCTTCTTCGGCCCTGAAGGGCTCACCACCAGCGGGGGGAACCGGTGCAGGGGGTCTACGGCTT
DNAPTAO		.....CA.....G..G.....
DNAPTFL		.....T.....C.....C.....C..T.....
DNAPTTH		.....G.....
MAJORITY		CGCCAAGAGGCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGGCGGTGXTGTGTGTCTTTGAGCGCCAAG
DNAPTAO		.....C.....A.....
DNAPTFL		.....A.....GT..T.....
DNAPTTH		.....T..AA...C..CT.....
MAJORITY		GGCGCTCTCTTCGGCCAGAGGCTACGAGGCTACAAGCGCGGGCGGGCCCCCAGCGGAGGACTTTC
DNAPTAO		.....G..GG.....G.....
DNAPTFL		.....
DNAPTTH		.....GA.....G.....C.....C.....
MAJORITY		CGCGGCAGCTCGGCTCATCAAGGAGCTGGTGGACCTCCTCGGGCTTGGCGGCTTCAGGTCCCCGGCTA
DNAPTAO		.....A.....G.....G.....
DNAPTFL		.....G.....T.....A..C.....T...G..G.....T.....
DNAPTTH		.....T.....T..A..C.....

**FIG. 2B**

FIG. 2C

MAJORITY [SEQ ID NO:7]	TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGAGCTATCCAGGTGGCAGCGACCTGCCCTGGCA	
DNAPTAO [SEQ ID NO:1]	....T.....C..T...A.....C..GG..A.....	764
DNAPTEL [SEQ ID NO:2]	....GGG.....G..C....GCC..T...C..A...T.....A...T.....	761
DNAPTTH [SEQ ID NO:3]	....A.....C.....A.....C..G.....T.....C...G.....C.....	770
MAJORITY	GGTGGACTTCGCCAAGXGGGGGAGGCGCGACCGGAGGGGCTTAGGGCCTTCTGGAGAGCGCTGGAGTTT	
DNAPTAO	.....AA.....A.....A.....	834
DNAPTEL	.....GG..G..C..C..CACA...A...T.....T..GG...T...T.....C..T.....	831
DNAPTTH	.....C.....C..G.....	840
MAJORITY	GGCAGCGCTCCTCCACGAGTTCGGGCTCCTGGAGGGCGCCCAAGCGCGCTGGAGGAGGGCCCCCTGGCCCCCGCG	
DNAPTAO	.....T.....AA.....	904
DNAPTEL	..A.....G.....G.....G..G....GGCA.....T..	901
DNAPTTH	.....C.....G.....GCGC.....	910
MAJORITY	GGCAAGGGCGCTTCCTGGGCTTGTCCCTTCCGGCGCCGAGCGCCATGTGGCGCGAGCTTCTGGCGCCTGGC	
DNAPTAO	.....G.....AAG.....T.....	974
DNAPTEL	.....T..Tt.....TC..T.....T.....	971
DNAPTTH	.....C.....C.....G.....AAA.....	980
MAJORITY	CGCGCGCAGGGAGGGCGGCTCCACCGGGCAGCAGACCCCTTTAXGGGCGCTXAGGGAGCCTXAAGGAGGTG	
DNAPTAO	.....G.....C..C..G..T..A..AA..C...C.....G.....C..	1044
DNAPTEL	T..GG..GT.....G..CC...T.....A.....C...G.....G.....T....G....	1041
DNAPTTH	.....TQ.....C.....G.....G.....GCG...G..A..A.....C.....C.....C..	1050

FIG. 2D

```

MAJORITY [SEQ ID NO:7]  CCGGGGXCCTGCTGGCCAGGACCTGGCCGTTTGGCCCTGAGGGAGGGCCCTXGACCTCTGCCCCGGGGAGCG
DNAPTAQ [SEQ ID NO:1]  .....G..T.....A.....AG....C.....A.....T.G....CC.....C.... 1174
DNAPTFL [SEQ ID NO:2]  .....AA....G.....G.....G.....C.....T.C...A.A..... 1181
DNAPTTH [SEQ ID NO:3]  .....C.....C.....C.....TC.....G.A.....G..... 1190

MAJORITY  ACCCGCATGCTGCTGGCCTACCTGCTGGACCCCTGCAACACACCCCGGAGGGGGTGGCCCGGGCGCTACGG
DNAPTAQ .....T.....T..... 1184
DNAPTFL .....T.....T..... 1181
DNAPTTH .....G.....G..... 1190

MAJORITY  GGGGGAGTGGACGGAGGAXCGGGGGGAGCGCGCCCTGCTXTCGGAGAGGCTCTTCCXGAACCTXXGGAG
DNAPTAQ C.....G.....G.....GC...T.....GCC.....GTG..G. 1254
DNAPTFL .....T.....A.....GG.....C.G.....A..C...AAA.... 1251
DNAPTTH .....C..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

MAJORITY  CCGCCTTGAGGGGGAGGAGAGGCTCCTTGGCTTTACGAGGAGGTGGAGAGCCGCTTCCCGGGTCCCTGG
DNAPTAQ A.G.....A.....G.....G.....GCT..... 1324
DNAPTFL .....A....A..AC.C..G.....G.....G.....GT... 1321
DNAPTTH .....C.....A.....C.....C.....A.....G..... 1330

MAJORITY  CCCACATGGAGGCCACGGGGGTXCGGCTGGACCTGGGCTACCTCCAGGGCCCTXTCCTGGAGGTGGCGGA
DNAPTAQ .....G..C.....G..C.....T..AG....T.G.....C.. 1394
DNAPTFL ...GG.....C.....C.....C.....C.....A..C 1391
DNAPTTH .....C.....A.....A.....T.....T.....C.T..... 1400

```

FIG. 2E

MAJORITY [SEQ ID NO:7]	GGAGATCGGGCGGCTCGAGGAGGAGGCTTCCGGCTGGCGGGGCGACGGCTTCAACCTCAACTCCCGGGAC	
DNAPTAA [SEQ ID NO:1]	.....GC.....CC.....	1464
DNAPTFL [SEQ ID NO:2]	.....G.C....AG..G.....	1461
DNAPTTH [SEQ ID NO:3]	.....T.....G.....	1470
MAJORITY	CAGCTGGAAAGGCTGCTCTTTGACGAGGCTXGGGCTTCCCGCCATCGGCAAGAGCGGAGACXGGCAAGC	
DNAPTAA	.....C.....A.....C.....	1534
DNAPTFL	.....GC.....G.C..G..T.....	1531
DNAPTTH	.....TA.....T.G..G.....	1540
MAJORITY	GCTCCACGAGCGCGCGCTGCTGGAGCGGCTXCGXGAGGGCGCCACGGCCATCGTGGAGAGATCCTGCAGTA	
DNAPTAA	.....C.....C..C.....	1604
DNAPTFL	.....T.....G..A.....CGGC.....	1601
DNAPTTH	.....G.....A..G.....C...C..	1610
MAJORITY	CGCGGAGCTCACCAGGCTCAAGAACACGCTACATXGACCGCGCTGCCXGXGCTCGTCCACGCCAGGACGGGC	
DNAPTAA	.....G...G.....T.....G.A....A.....	1674
DNAPTFL	.....A.....C.C...G.....A...C...C...	1671
DNAPTTH	.....G.C.....G..AAG.....G.....	1680
MAJORITY	CGGCTCCACACCGCGCTTCAACGAGACGGCGCAGCGGCGAGGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAA	.....A.....A.....T.....C..	1744
DNAPTFL	.....G.....C.....TCC.....	1741
DNAPTTH	.....G.....G.....	1750

FIG. 2F

MAJORITY [SEQ ID NO:7]	AGAACATCCCGCTCCGACGCCGCTGGGCCAGAGGATCCGCCGGGCTTCGTGGCCGACGAGGGTGGGT	
DNAPTAQ [SEQ ID NO:1]	.....G..T..G.....A..C.....G....C..1814	
DNAPTFL [SEQ ID NO:2]	.....G.....T.....C..C.....A.....C.....C....1811	
DNAPTTH [SEQ ID NO:3]	.....CT.....CT.....C...T....G1820	
MAJORITY	GTTCGTGGCCCTGGACTATAGCCACATAGAGCTCCGGGTCCTGGCCCACTCTCCGGGACGAGAACCTG	
DNAPTAQ	A.....A.....G.....C.....1884	
DNAPTFL	.....T..T.....C.....T.....1881	
DNAPTTH	.....C.....C.....C.....A.....1890	
MAJORITY	ATCCGGGCTTCCAGAGGGGAGGACATCCACACCCAGAGCCGCCAGCTGGATGTTCGGCGTCCGCCCGG	
DNAPTAQ	.....C.....GG.....G...1954	
DNAPTFL	.....T.....T.....TT....G..1951	
DNAPTTH	.....A.....A.....A.....1960	
MAJORITY	AGCCCGTGGACCCCTGATGCCCGCGGGCCAGACCATCAAGTGGGGTCTCTACGGCATGTCCGC	
DNAPTAQ	.....G...2024	
DNAPTFL	.....A..G..A....T.....G.....2021	
DNAPTTH	.....GG..G.....G.....2030	
MAJORITY	CCACCGGCTCTCCAGGAGCTTGGCATGGGTAGGAGGGGGTGGCCTTCATTGAGCGGTACTTCCAG	
DNAPTAQ	.....A.....T.....CCA.....T...2094	
DNAPTFL	.....GG.....T.....2091	
DNAPTTH	.....TA..G.....T...A.....A2100	



FIG. 2G

MAJORITY [SEQ ID NO:7] AGCTTCCCAAGCTGGGGGCTGGATTGAGAAGACCCCTGGAGGAGGGCAGGAGGGGGGTACGTCGAGG 2164  
 DNAPTAQ [SEQ ID NO:1] ..... 2161  
 DNAPTFL [SEQ ID NO:2] .....T..... 2170  
 DNAPTTH [SEQ ID NO:3] .....A.....A.....C.....A..... 2170

MAJORITY CCCTCTCGGGCGCGGGGTACGTGCCCGACCTCAACGCCCGGGGTGAAGAGCGTCCGGCAGCGCGCGGA 2234  
 DNAPTAQ .....C.....A.....AG.C.....C... 2231  
 DNAPTFL .....T.....G.....C..... 2240  
 DNAPTTH .....AA.AA.....CA.....C..... 2240

MAJORITY GCGCATGCGCCTTCAACATGCCCCGTCCAGGGCACCGCGCGGACCTCATGAAGCTGGCCATGGTGAAGCTC 2304  
 DNAPTAQ .....T..... 2301  
 DNAPTFL .....G.....CG...T 2310  
 DNAPTTH .....C.....C..... 2310

MAJORITY TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCACGACGAGCTGCTCCTCGAGGGCCC 2374  
 DNAPTAQ .....A.....GG.....T..... 2371  
 DNAPTFL .....T.....C.....G.....TT.G.....G..... 2380  
 DNAPTTH .....C..C.G..G.....C.C.....C.....CC...G..... 2380

MAJORITY CCAAAGAGCGGGCGGAGGXGGTGGCCGCTTGGCCCAAGAGGTCATGGAGGGGCTCTATCCCTCGGCGCT 2444  
 DNAPTAQ .....A.....CC.....CGGC.....G..... 2441  
 DNAPTFL .....G..C.....AG...A.....GG.....CAG.. 2450  
 DNAPTTH .....C....C.....C....A.....G.....C.....AA..C.....C..... 2450

FIG. 2H

MAJORITY [SEQ ID NO:7]	GCCCGTCGAGGCTGGAGCTGGGGATCGGGGAGGACTGGCTCTCGGCCAAGGAGTAG
DNAPTAQ [SEQ ID NO:1]	.....A.....GA
DNAPTFL [SEQ ID NO:2]	.....CC.....
DNAPTTH [SEQ ID NO:3]	.....T.....GT...

10074923.05.1.2002

FIG. 3A

MAJORITY [SEQ ID NO: 8]	MXAMLPLEFPKGRVLLVDGHHLAYRTFFALKGLTTSRGEPUQAVYGFAXSLLKALKEDG-DAVXVVFDAK	
TAQ PRO [SEQ ID NO: 4]	.RG.....H.....I.....	69
TFL PRO [SEQ ID NO: 5]	.....V.V.....	68
TTH PRO [SEQ ID NO: 6]	.E.....YK..F.....	70
MAJORITY	APSFRAHEAYKACRAPTPEDFPROLALI KELVDLLGLXRLEVPQYEADVLATLAKKAEKEGYEVRIL	
TAQ PRO	GG.....A.....S.....	139
TFL PRO	.....V.....F.....R.....	138
TTH PRO	.....FT.....	140
MAJORITY	TAORDLYQLLSDRI AVLHPGYLITPAWLWEKYGLRPEQWVDYRALXGDPDSNLPQVKGI GEXTAXKLLX	
TAQ PRO	...K.....H.....D..A.....T..E.....R...E 209	
TFL PRO	.....E...I.....Y.....A.....I.....GR..IR 208	
TTH PRO	...V...V.....H...E.....F...V.....L...K 210	
MAJORITY	EWGSLNLLKNLDRVKP-XXREKIXAHMEDLXLSSXLSXVRTDLPLEVDFAXRREPDREGLRAFLERLF	
TAQ PRO	.....A.....L...AI...L...D...K...WD.AK.....K.....R.....	278
TFL PRO	.....FQH...O...SL...IQ.G...A.A...RK..Q.H.....GR..T.NL.....	277
TTH PRO	.....ENV...K..L...R...LE..R.....L.OG.....	280
MAJORITY	GSLLHEFGLLLEXPKALEEAPWPPPEGAFVGVLSRPEPMWAEALLAAXRGRVHRAXDPLXGLRDIKEV	
TAQ PRO	.....S.....K.....D.....G.....PE.YKA.....A 348	
TFL PRO	.....G...A.....L..SF.....G.WE..L...Q...R.....G. 347	
TTH PRO	.....A.AP.....K...C.D.....A...A...K..... 350	

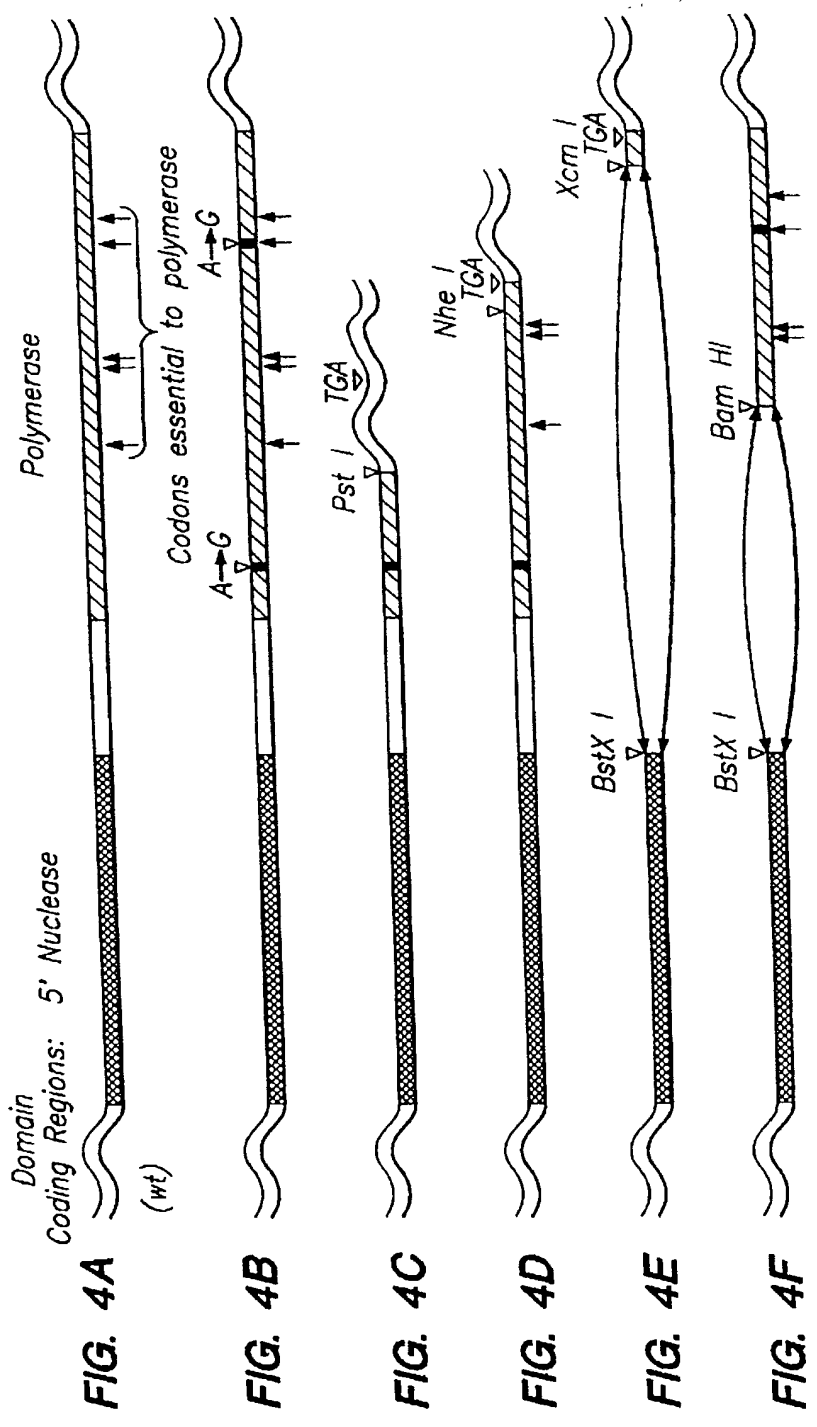
FIG. 3B

MAJORITY [SEQ ID NO: 8]	RGLLAKDLAVLALREGDLXPDDPMLLAYLLDPSNTTPEGVARRYGGWTEADAGERALLSERLFXNLXX	
TAQ PRO [SEQ ID NO: 4]	S.....G.P.....	E.....A.....A...WG 418
TFL PRO [SEQ ID NO: 5]	I.....F.E.....	A.....A.....QT.KE 417
TTH PRO [SEQ ID NO: 6]	S.....V.....	AH.....HR..LK 420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEI RRLEEEVFRLAGHPFNLSRD	
TAQ PRO	R...R...A.....R.....A...A.....	488
TFL PRO	K...E.....R.....EA.V.O.....	487
TTH PRO	K...H.....L.....	490
MAJORITY	OLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTCLKNTYIDPLPXLVHPRTG	
TAQ PRO		S.....D.I.....558
TFL PRO		DR.....A...K...557
TTH PRO	R...L...Q.....H.....V...S.....	560
MAJORITY	RLHTRFNOTATATGRLSSSDPNLQNI PURTPLGQRI RRAFVAEEGWXLVALDYSOIELRVLAHLSGDENL	
TAQ PRO		I.....L.....628
TFL PRO		V...V.....627
TTH PRO		A...A.....630
MAJORITY	IRVFOEGRDIHTQTASWMFGVPPAEVDPLMRRAAKTINFGVLVYGMSAHRLSOELAI PYEEAVAFI ERYFO	
TAQ PRO	E.....R.....	Q.....698
TFL PRO	S...G.....G...S.....	697
TTH PRO	K.....V.....	700

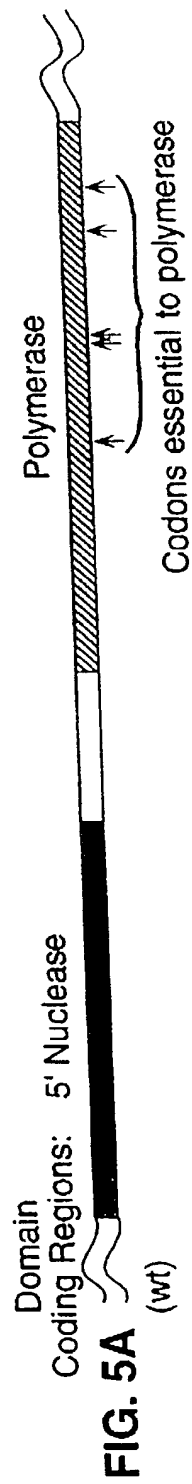
FIG. 3C

MAJORITY	[SEQ ID NO: 8]	SFPKVRAWI EKTLEGGRRRGYVETLFCRRRYVPDLNARVKSUREAERMAFNMPVQGTAAADLHKLAMVKL	768
TAQ PRO	[SEQ ID NO: 4]	.....E.....	767
TFL PRO	[SEQ ID NO: 5]	Y.....G.....R.	770
TTM PRO	[SEQ ID NO: 6]	.....K.....	
MAJORITY FPRLXEMGARM LLOVHDELVLLEAPKXRAEXVAALAKEVME GUYPLAVPLEVEVGXGEDWLSAKEX			
TAQ PRO	.....E.....E...A...R.....I.....	833	
TFL PRO	.....O.L.....D...R.....W.O.....L.....	831	
TTM PRO	.....R.....L...QA...E.....A..KA.....M.....G	835	

Genes for Wild-Type and Pol(-)DNAPTaq



# Genes for Wild-Type and Pol(-) DNAPTfl



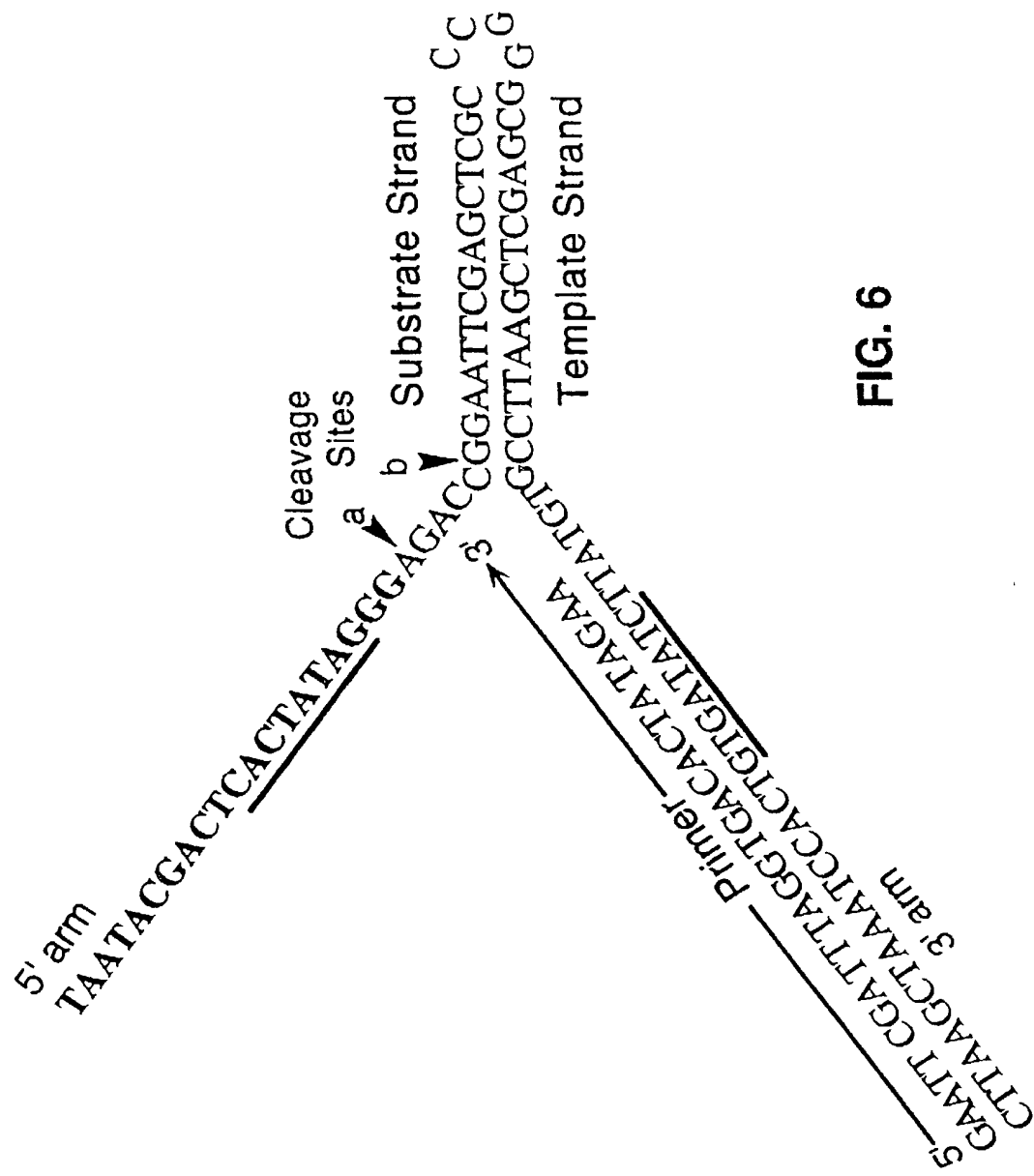
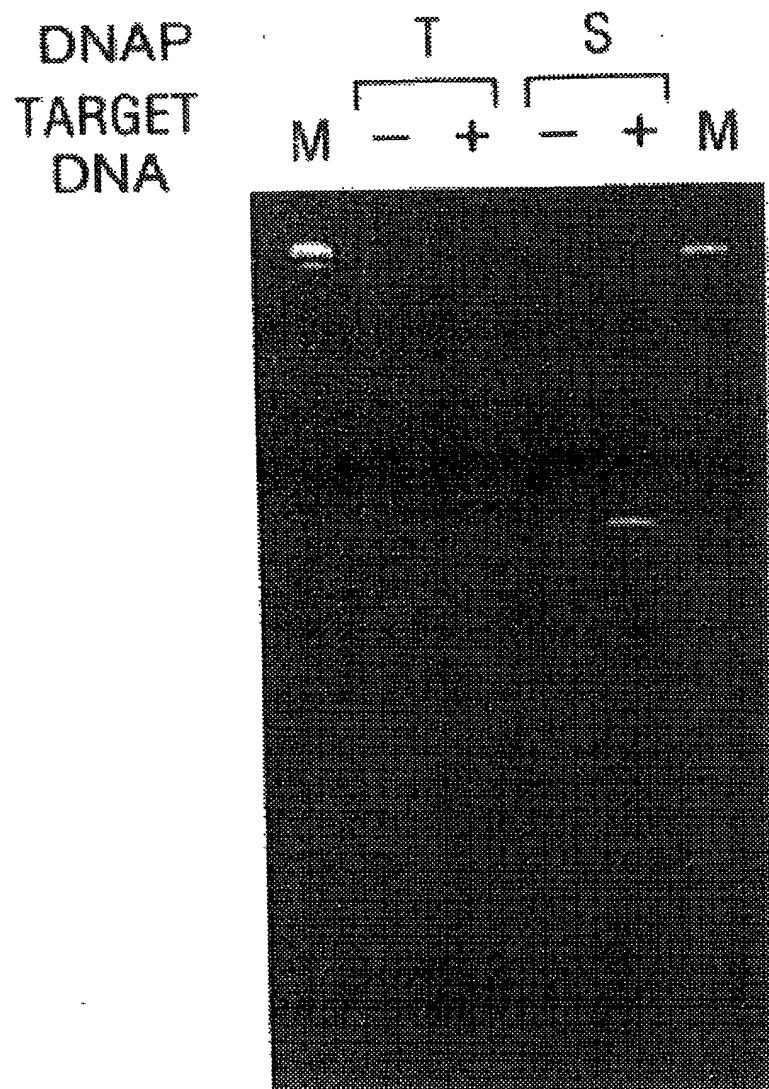


FIG. 6



**FIG. 7**

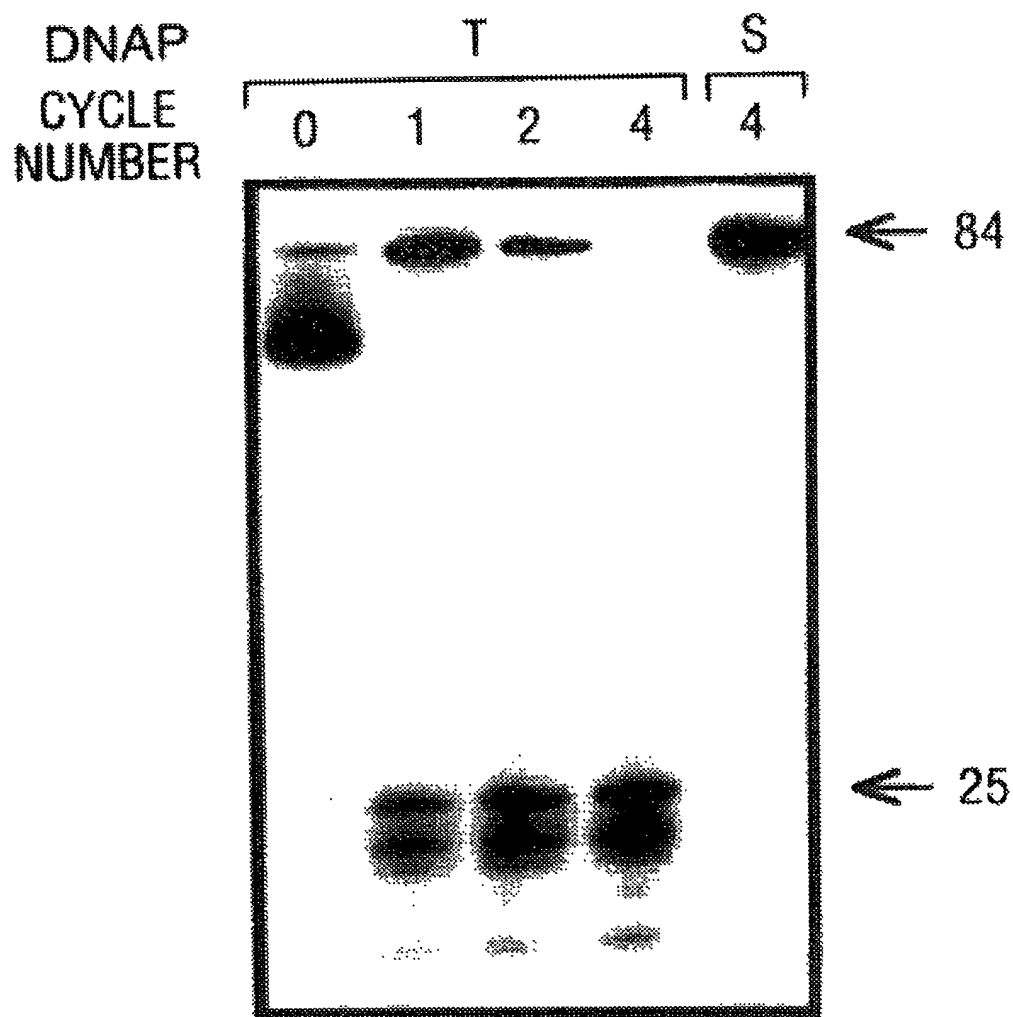


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

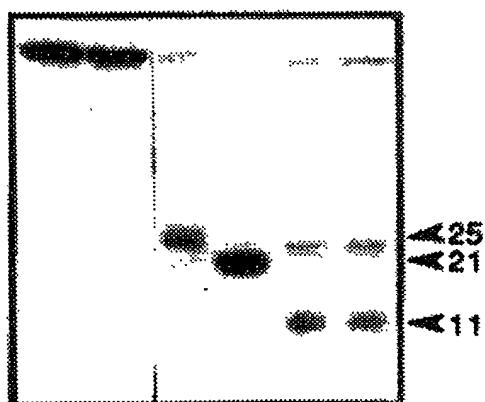
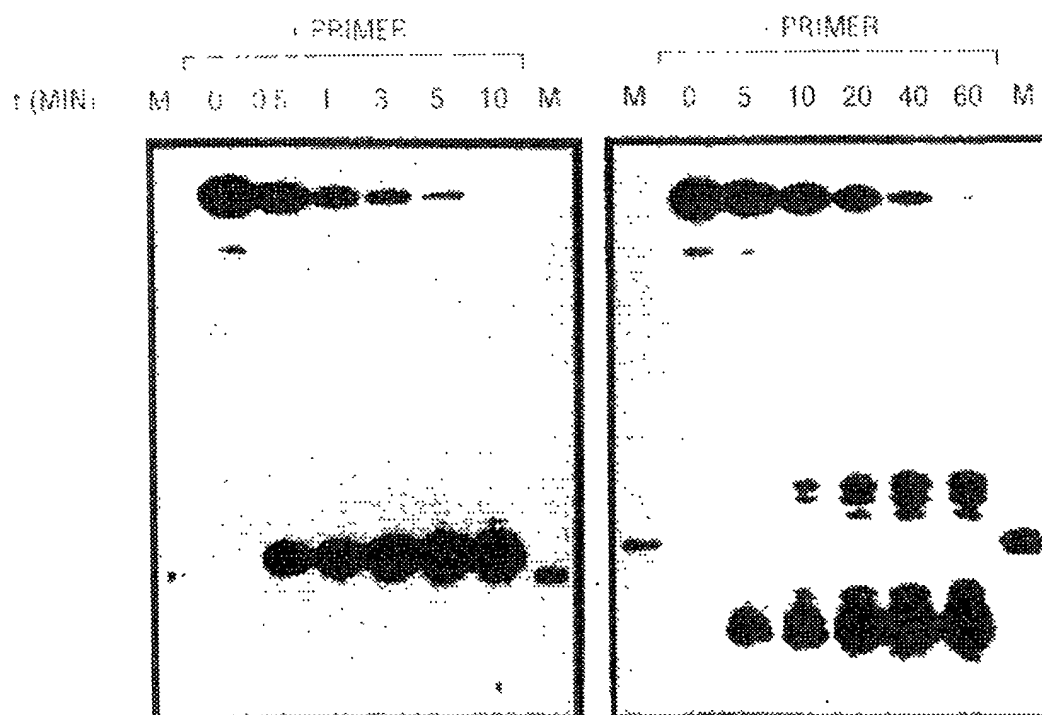
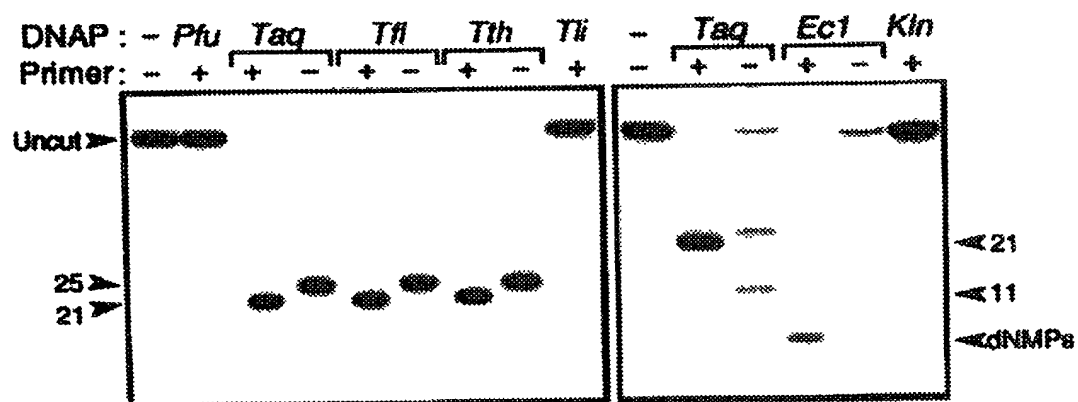


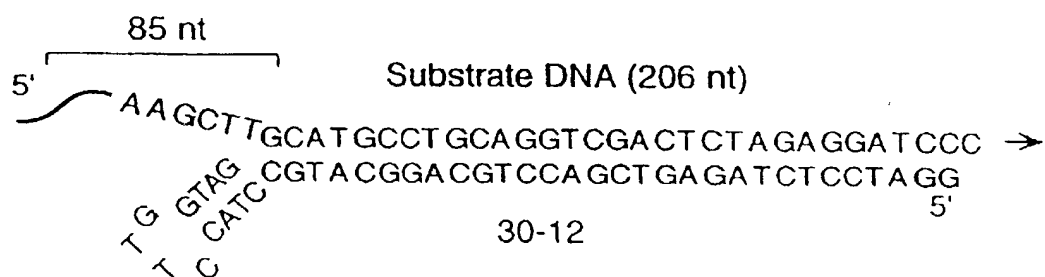
FIG. 9A

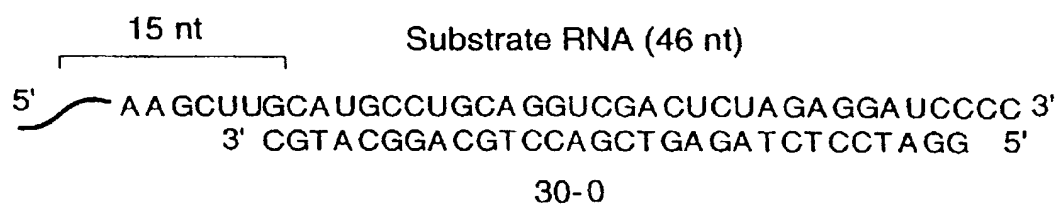


FIG. 9B









**FIG. 13A**

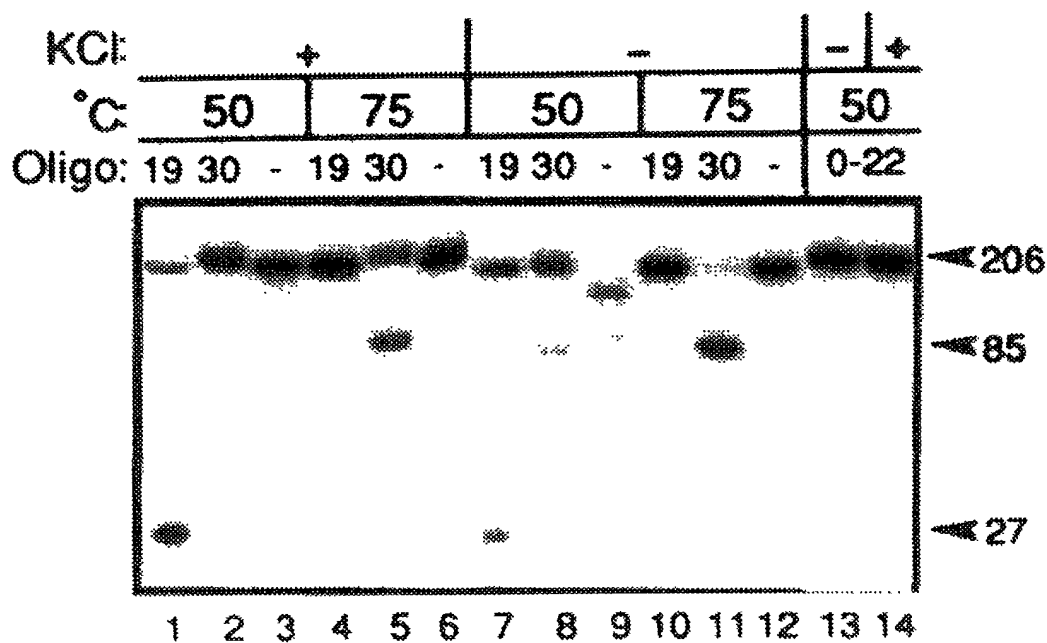


FIG. 12B

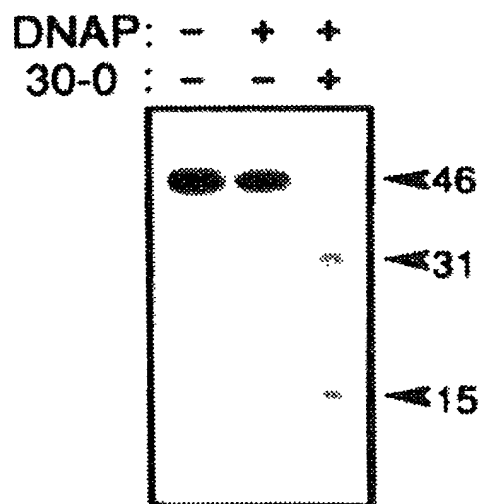
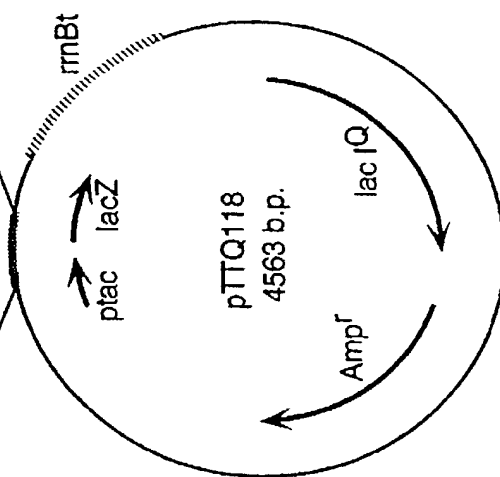


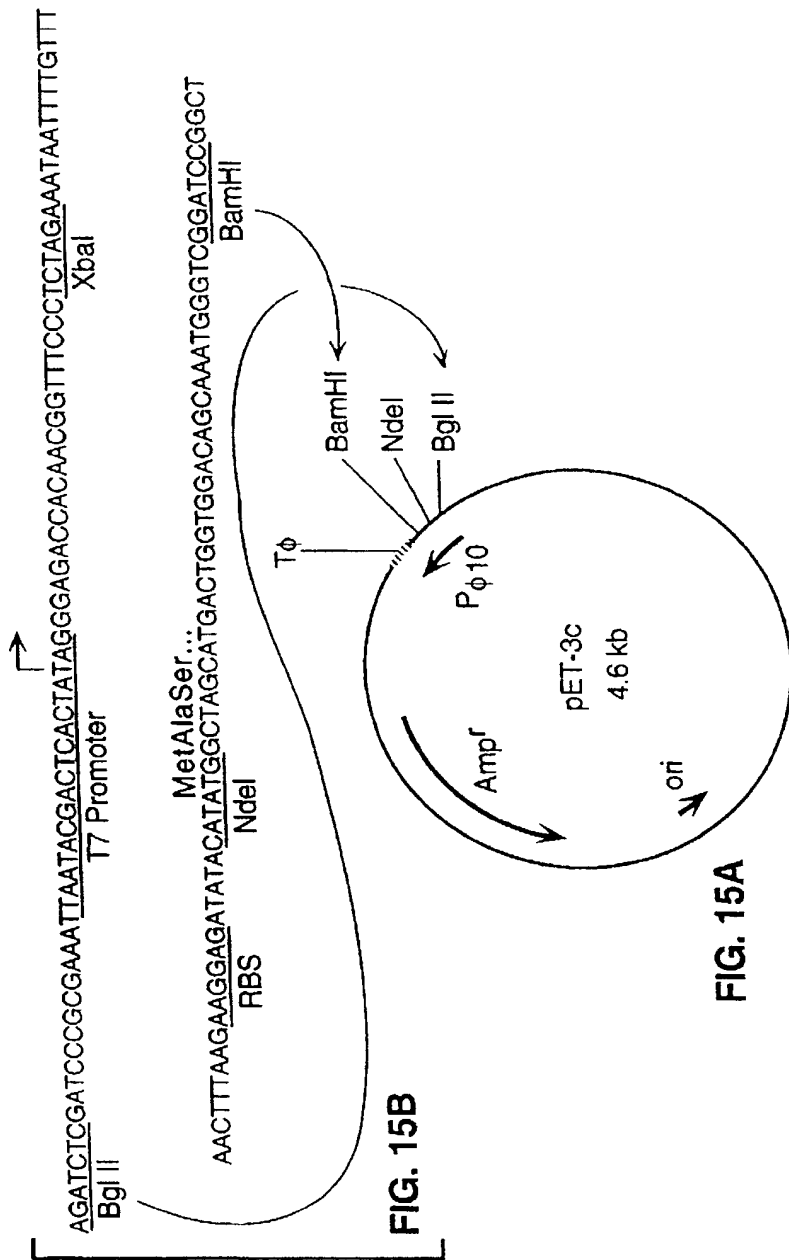
FIG. 13B



**FIG. 14B**



RBS: Ribosome binding site  
ptac: Synthetic tac promoter  
lac I<sup>Q</sup>: Lac repressor gene  
lacZ: Beta-galactosidase alpha fragment  
rmBt: E. coli mB transcription terminator



P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter  
Tφ: T7 φ Terminator  
RBS: Ribosome binding site

**FIG. 15C**

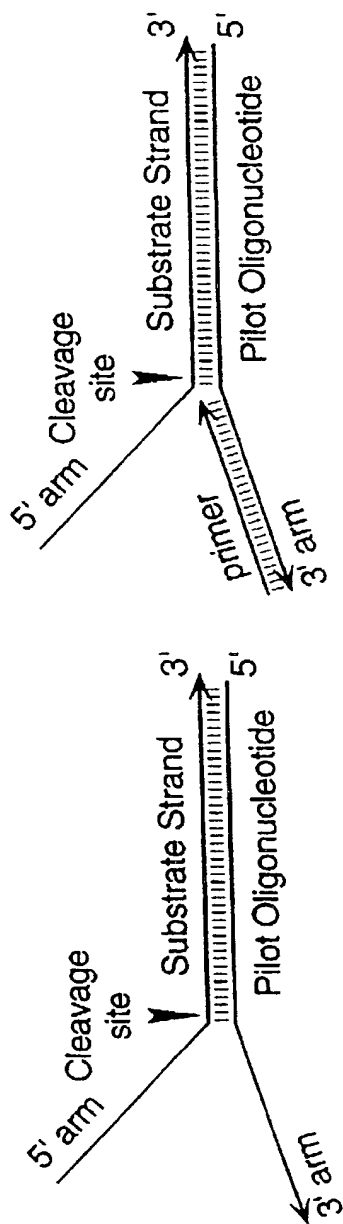


FIG. 16A

FIG. 16B

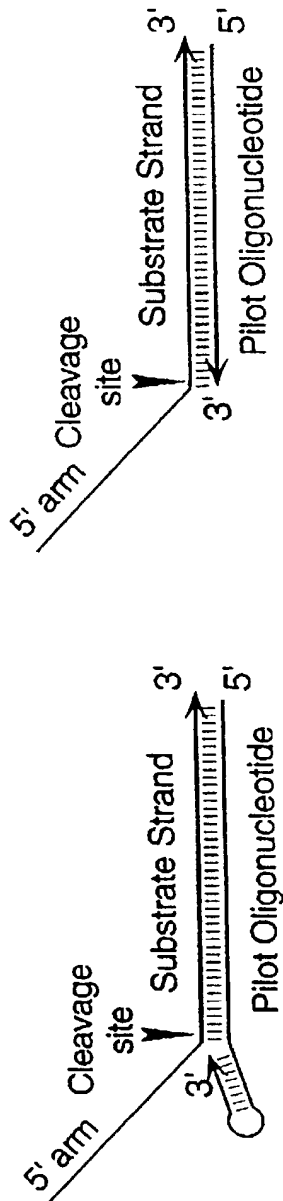


FIG. 16C

FIG. 16D

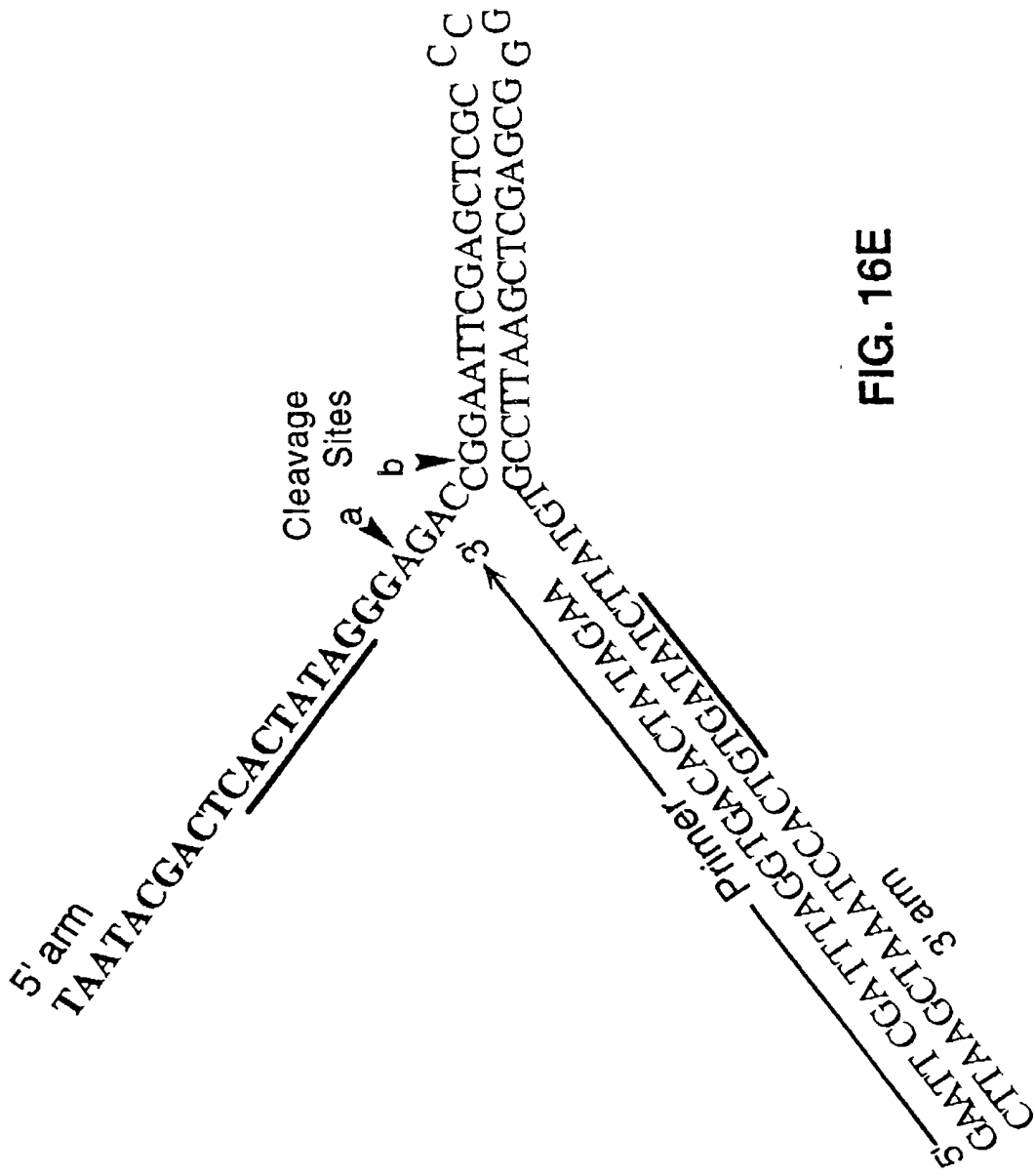


FIG. 16E

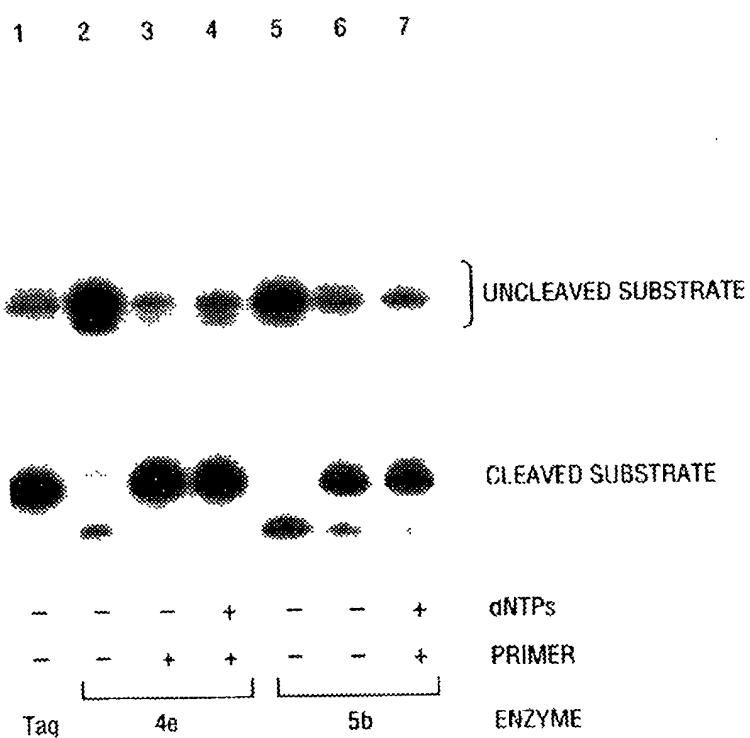


FIG. 17

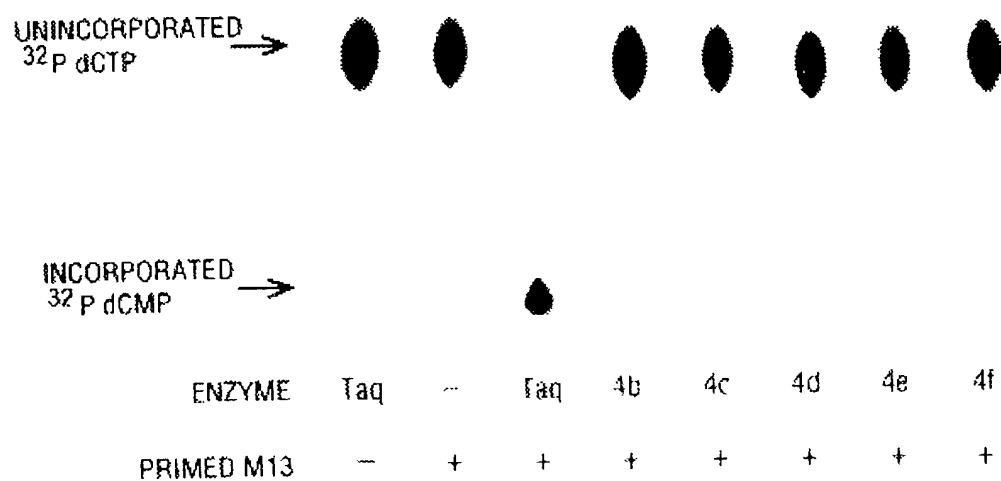


FIG. 18

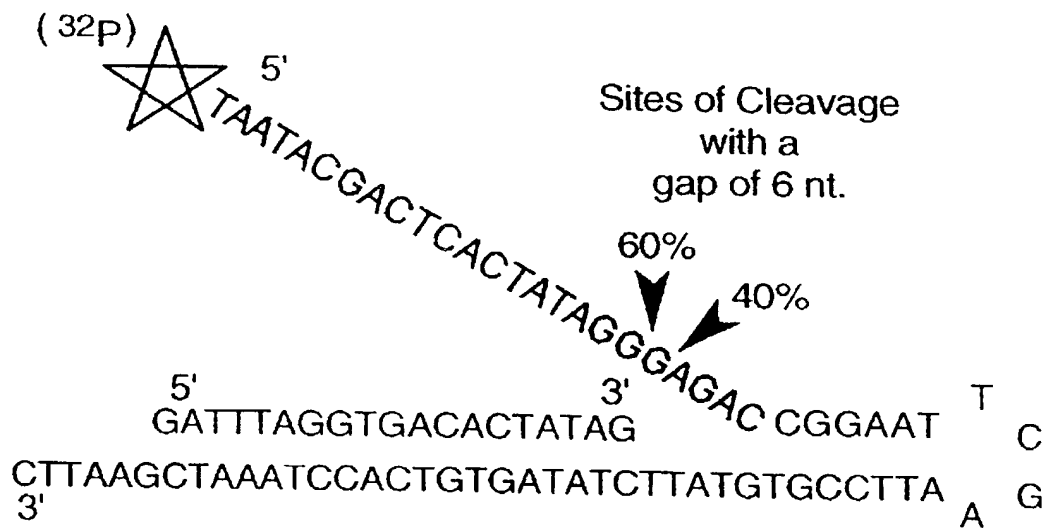
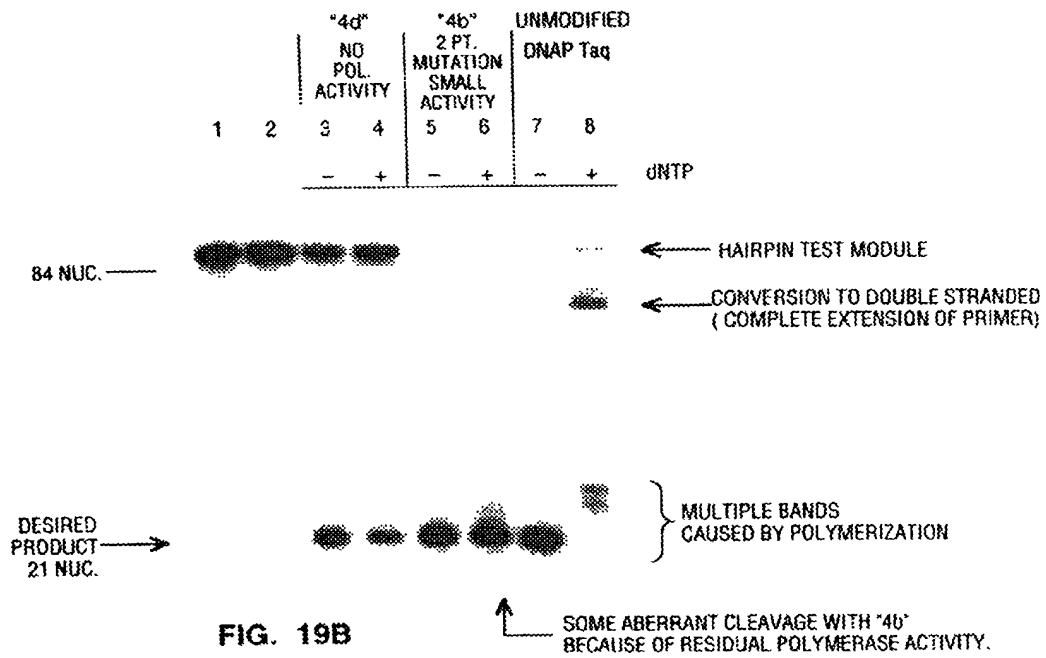


FIG. 19A



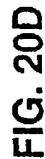




Sequence of alpha primer:

5' GACGAACAAGCGAGACAGCG 3'

**FIG. 20B**

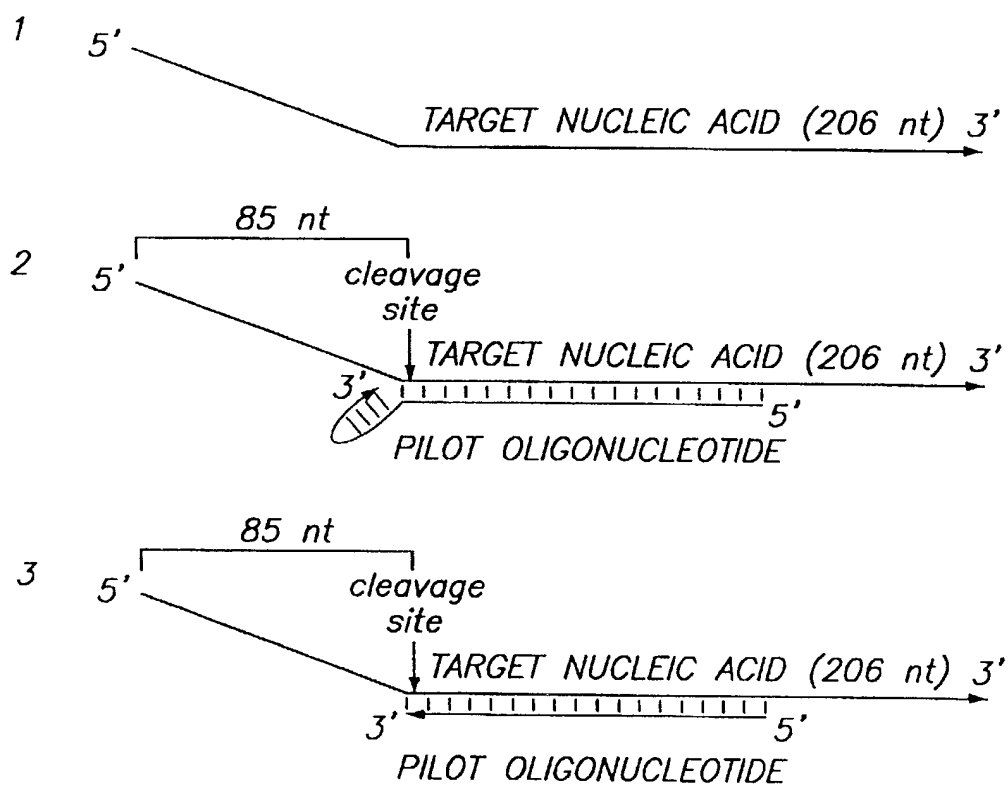


*Ban II*  
*Sst I*  
*Asp* 718  
*Ava I*  
*Kpn I*  
*Xma I*  
*Sma I*  
*Bam* *Hl* *Xl*  
*EcoR I*  
 CCGCAGGGTTTCCGAGTCAGAGCTTGTAACGACGGCCAGTGAAATTGTAATACGACTCACTATAGGGCGAATTCGAGCTCGGTACCGGGGATCCTC  
 GCGGTCCCAAAAGGTCAGTCGCAACAATTTGCTGCCGGTCACTTAACATTATGCTGAGTGAATATCCGCTTAAGCTCGAGCCAAGGCCCTTAGGAG  
 ——— -47 Forward ———  
 ——— 17 ———  
 ——— Pilot 30-0 ———

*Sal I*  
*Acc I*  
*Hinc II*  
*Pst I*  
*BspM I*  
*Sph I*  
*Hind III*  
 TAGAGTCGACCTGCAGGCCATGCAAGCTTGAGTATTCATAGTGTCACTAAATAGCTTGGCGTAATCATGGTCAATAGCTGTTCCCTGCTGAAATTTGTA  
 ATCTCAGCTGGACGTCGGTACGTTCCGAACCTCAATAGATATCACAGTGGATTTATCGAACCGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAAT  
 ——— Pilot 30-0 ———  
 ——— SP6 ———  
 ——— 2 ———  
 ——— -48 Reverse ———

TCCGCTCACAATTCACACACAATACGA 228  
 ACGGCACTGTTAAGGTGTTGTTATGCT  
 ——— -48 Reverse ———  
 ——— 206 ———

FIG. 21

**FIG. 22A**

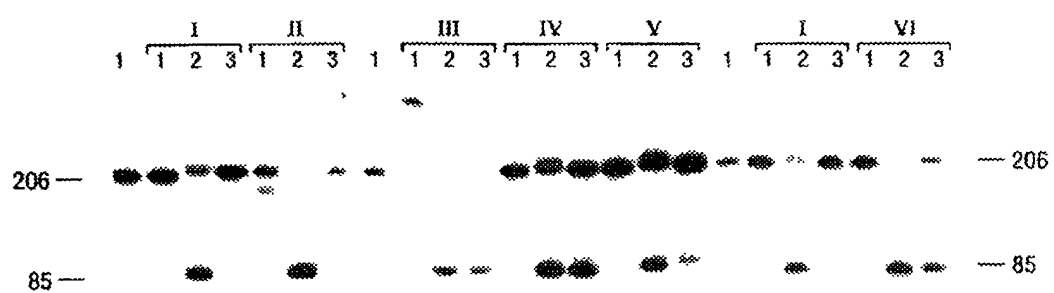


FIG. 22B

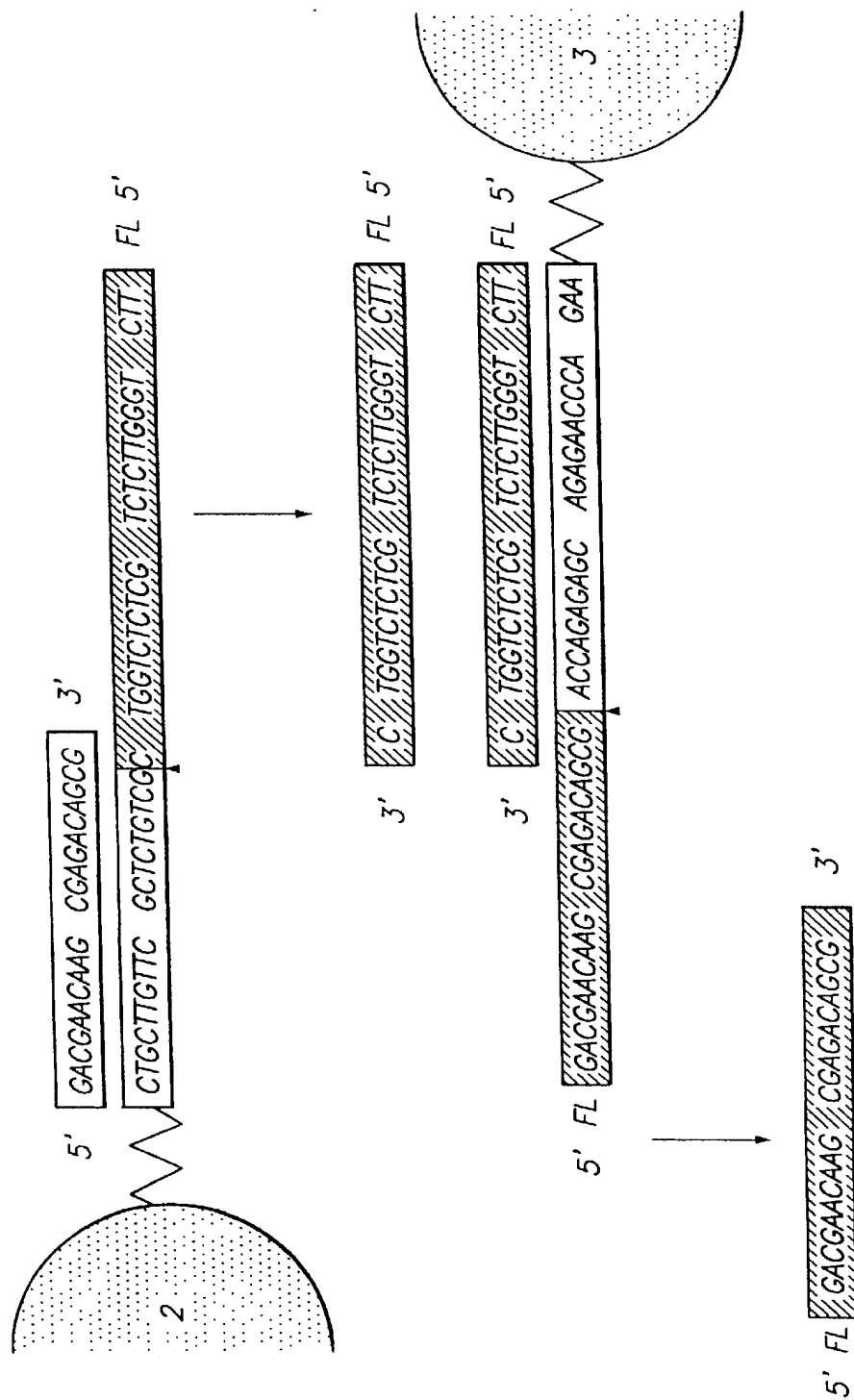


FIG. 23

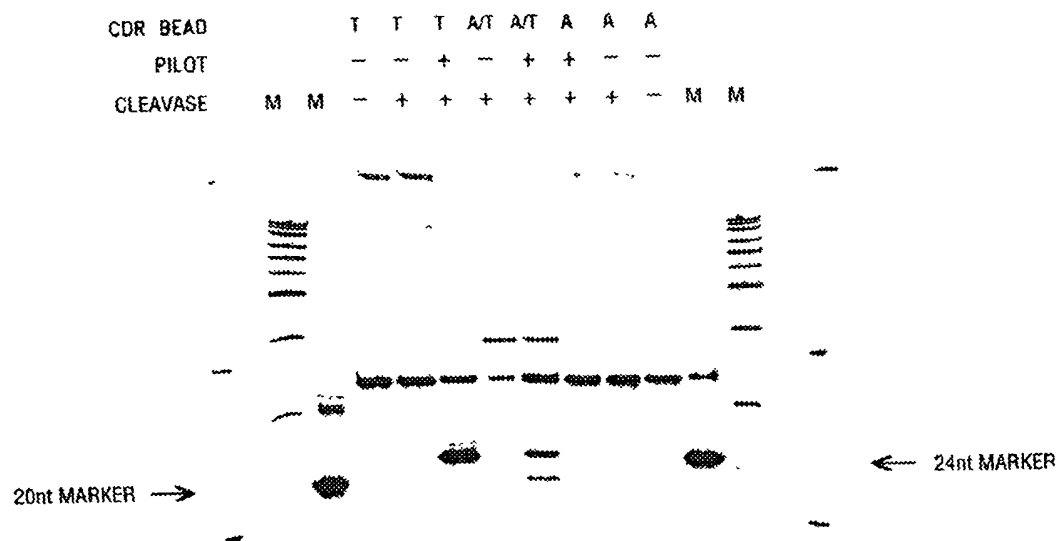


FIG. 24

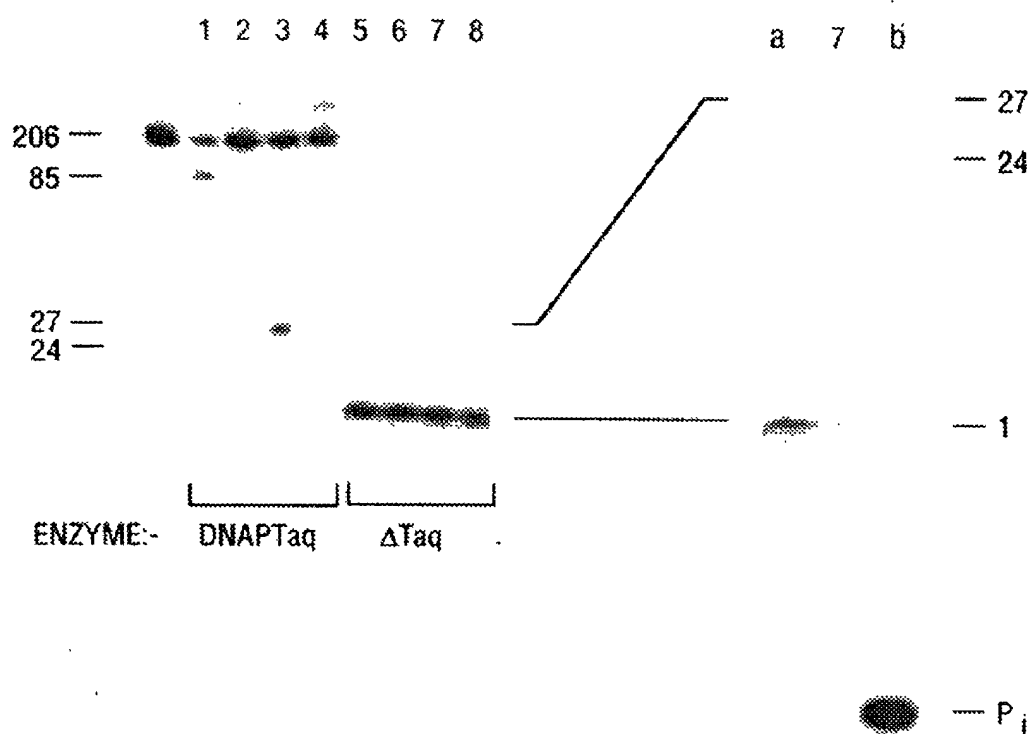


FIG. 25A

FIG. 25B

FIG. 26A

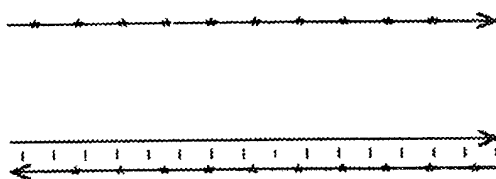
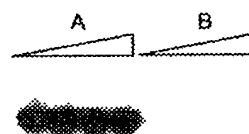
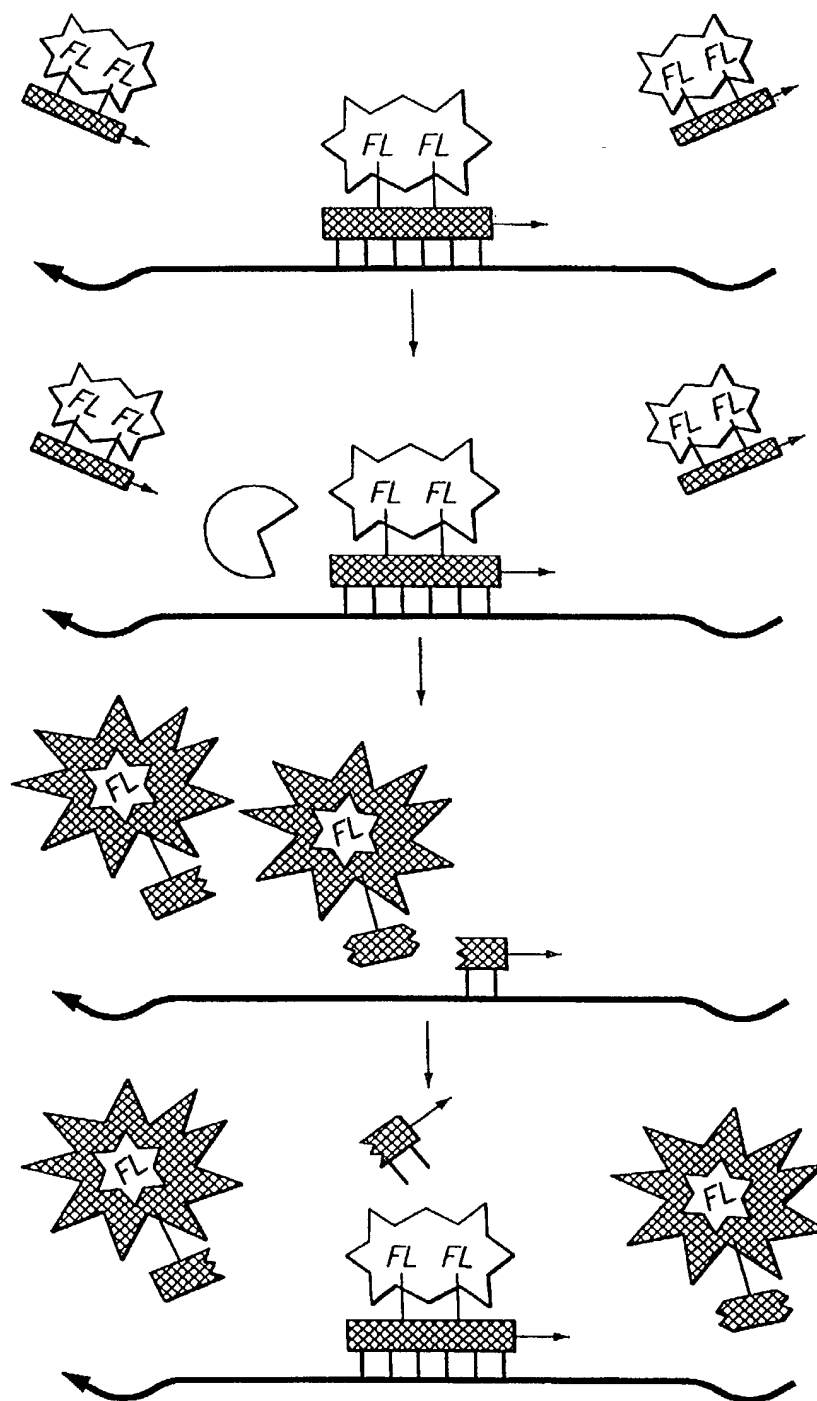


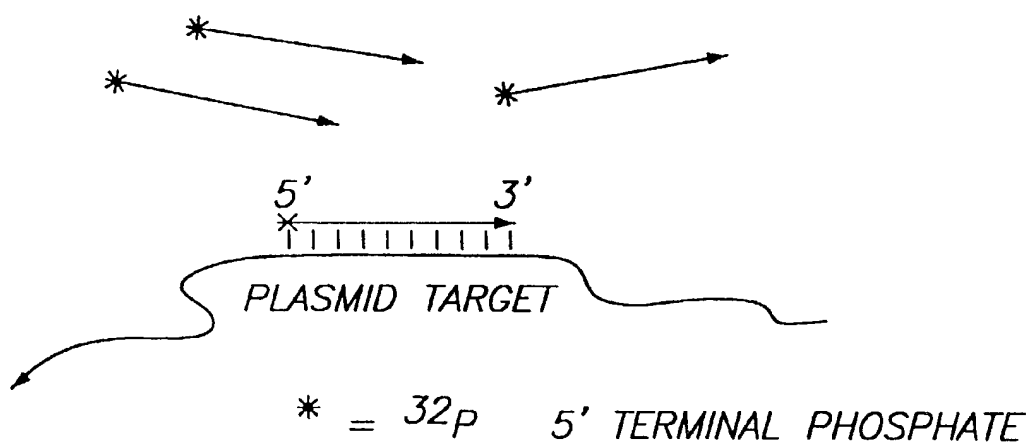
FIG. 26B

\* = 32p

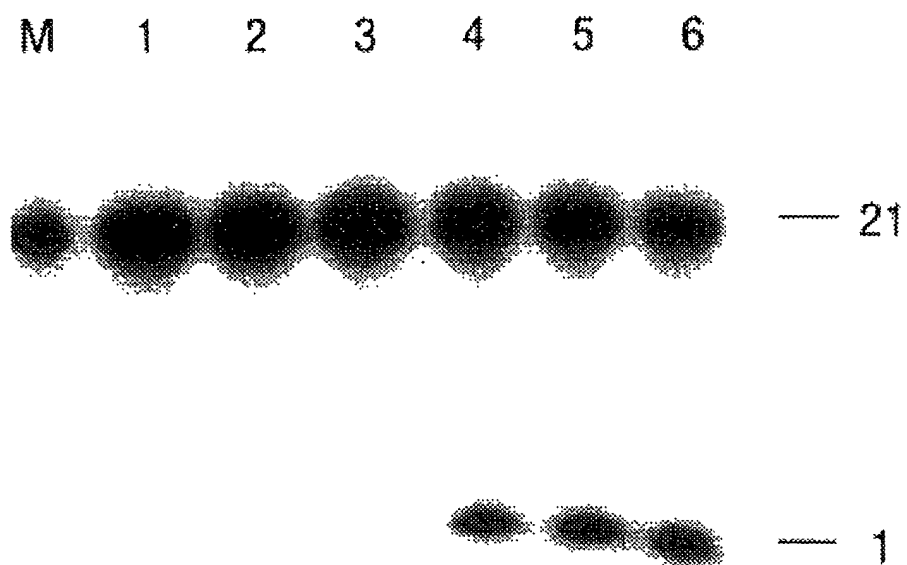




**FIG. 27**



**FIG. 28A**

**FIG. 28B**

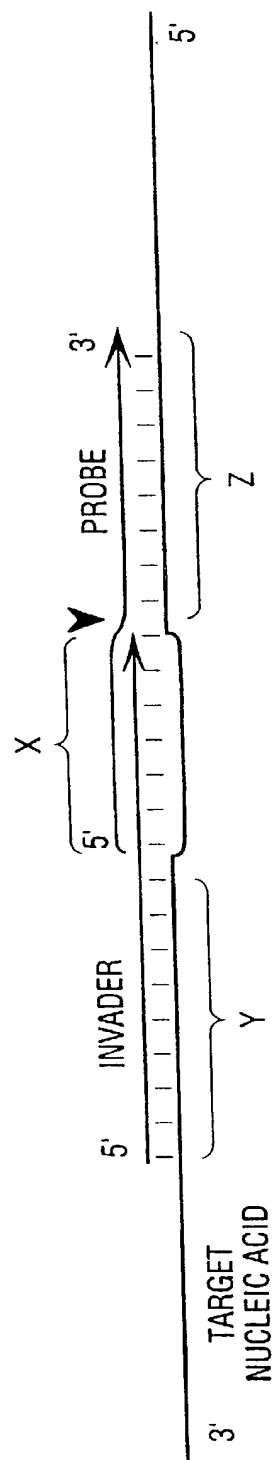


FIG. 29

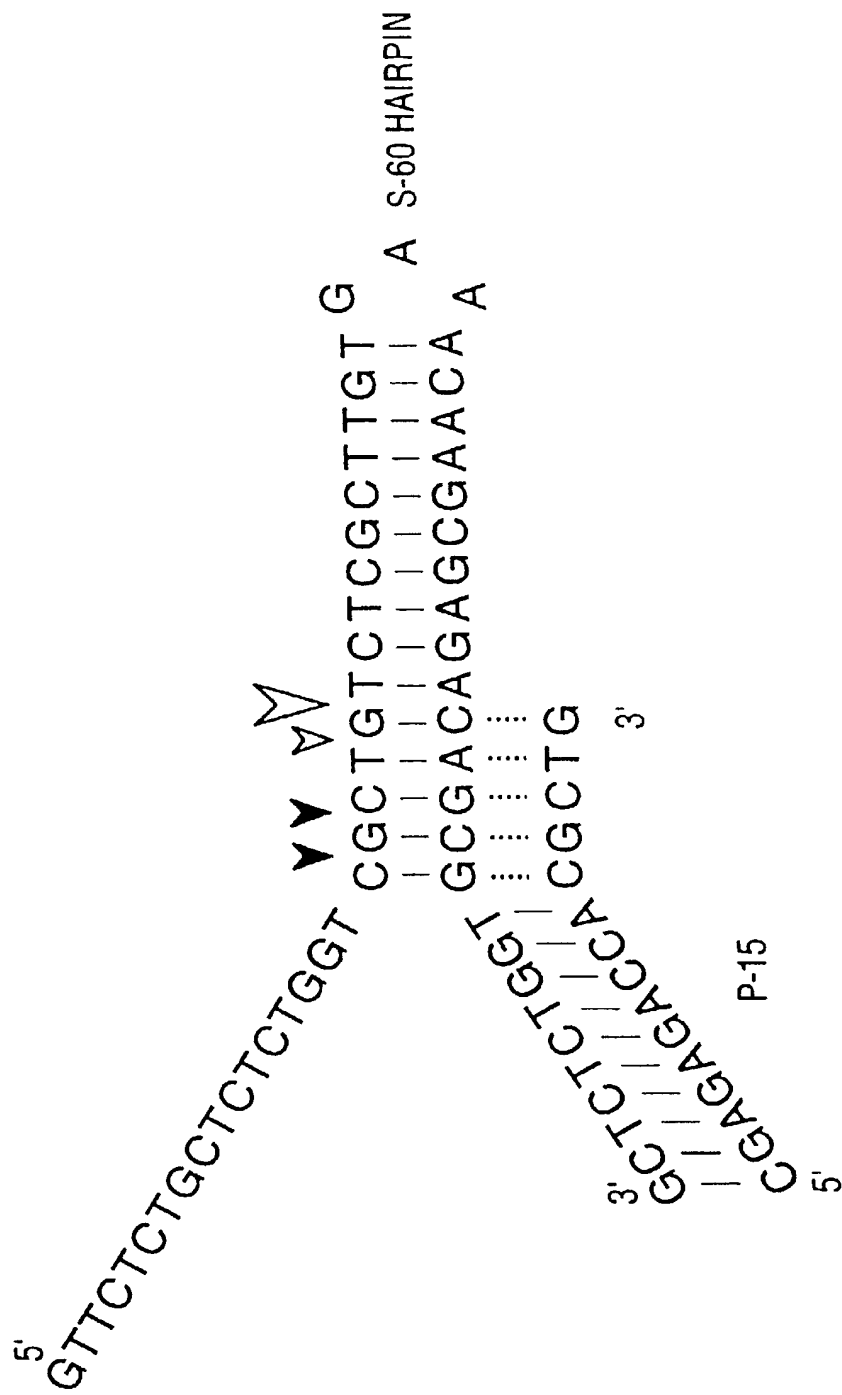
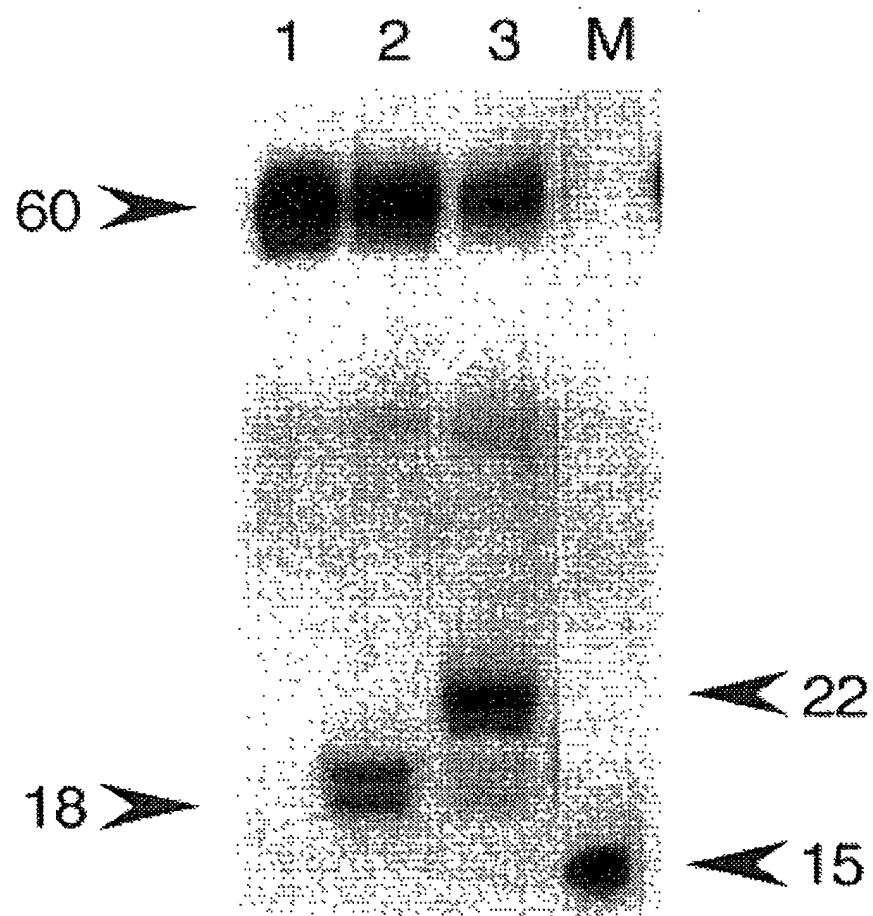


FIG. 30

**FIG. 31**

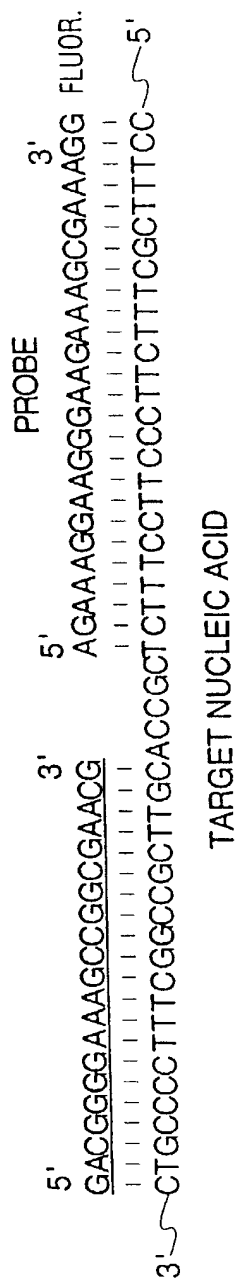


FIG. 32A

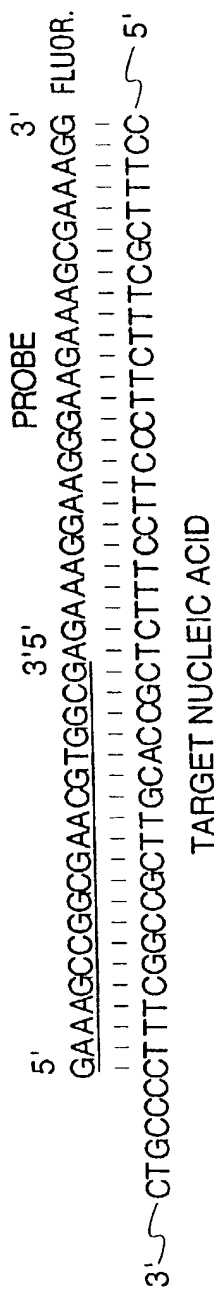


FIG. 32B

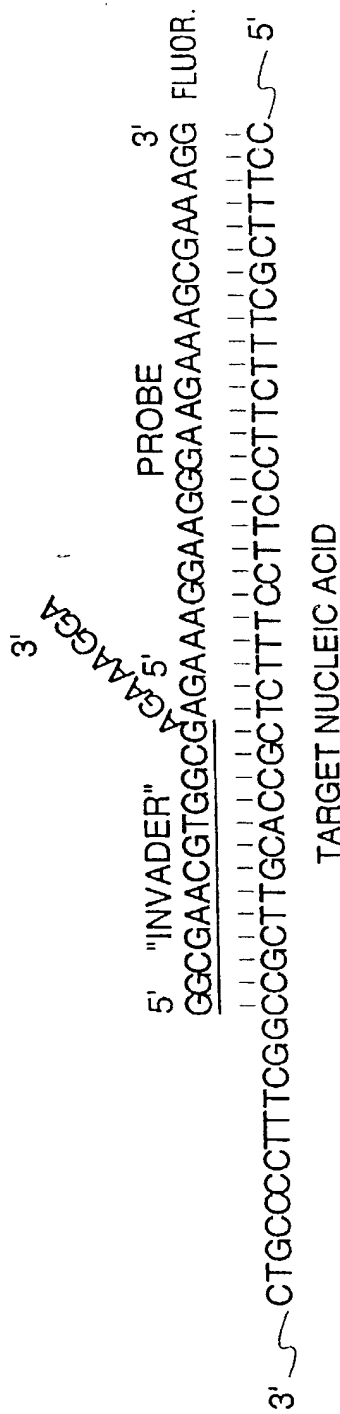


FIG. 32C

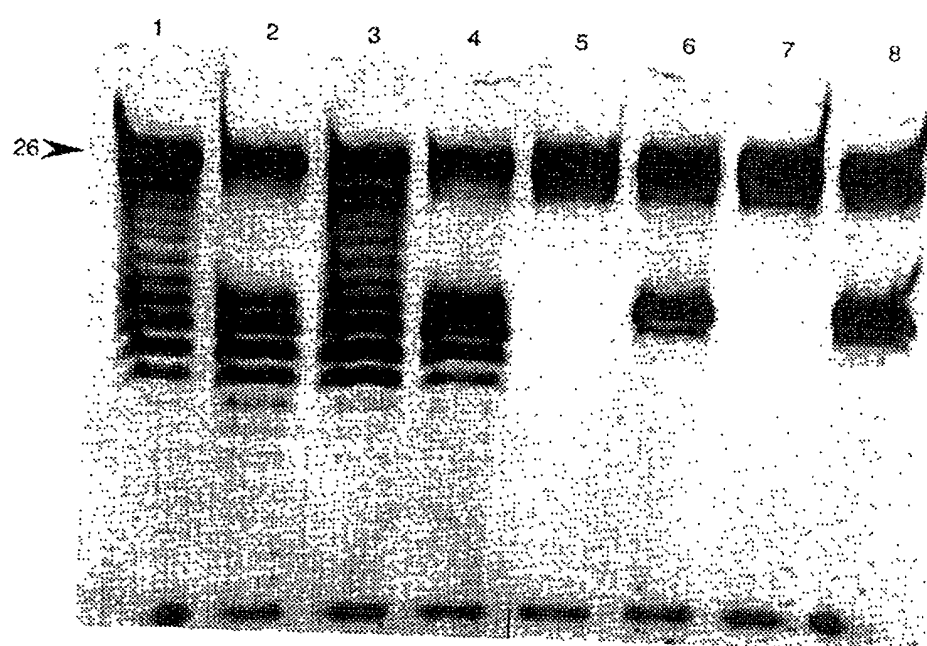


FIG. 33



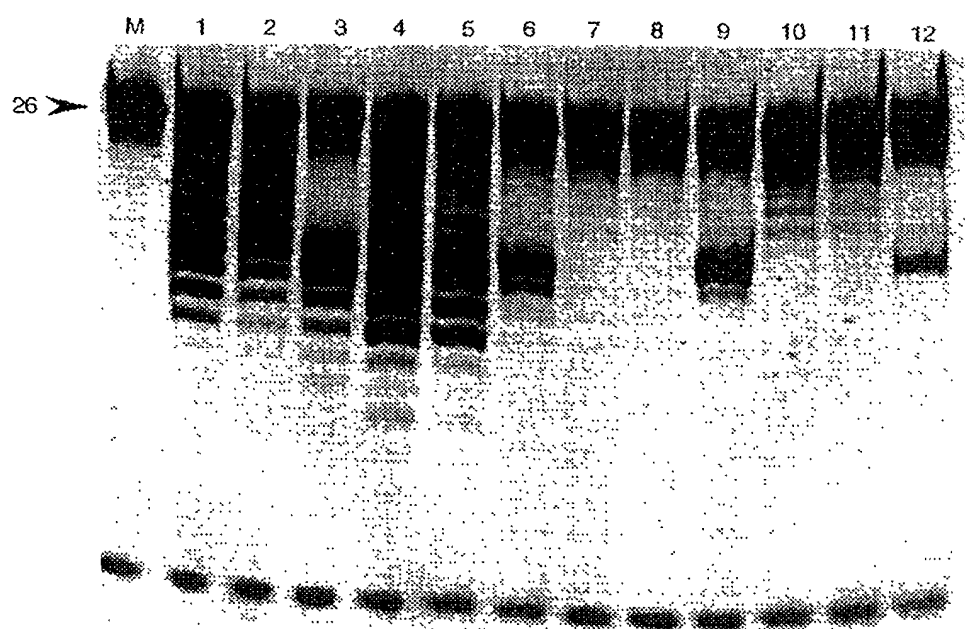


FIG. 34

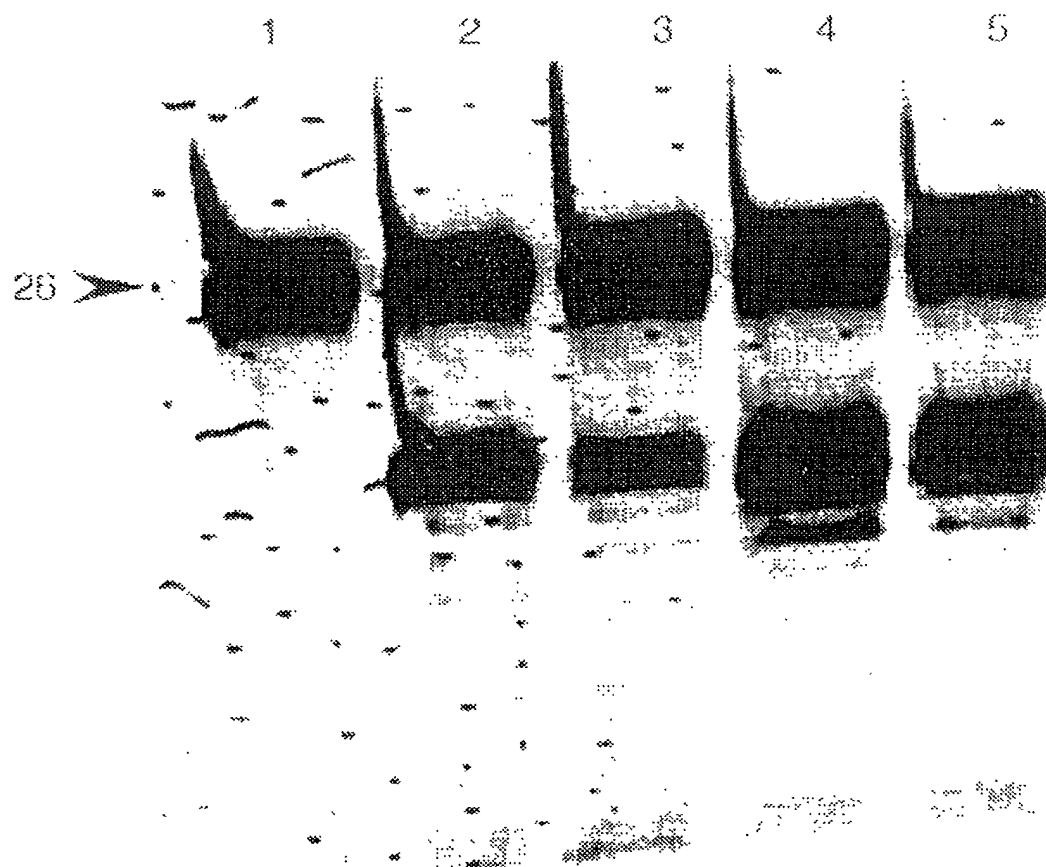


FIG. 35

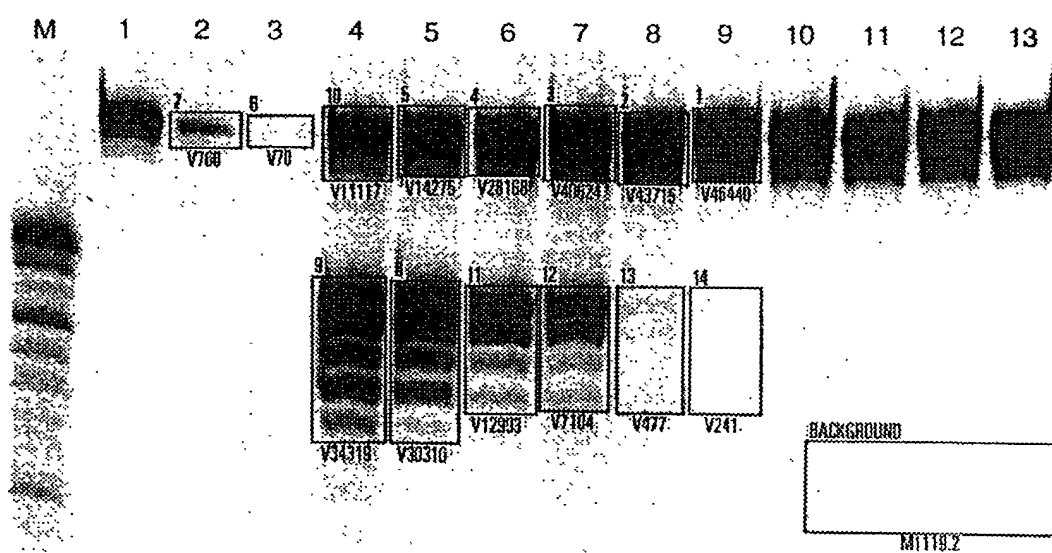


FIG. 36

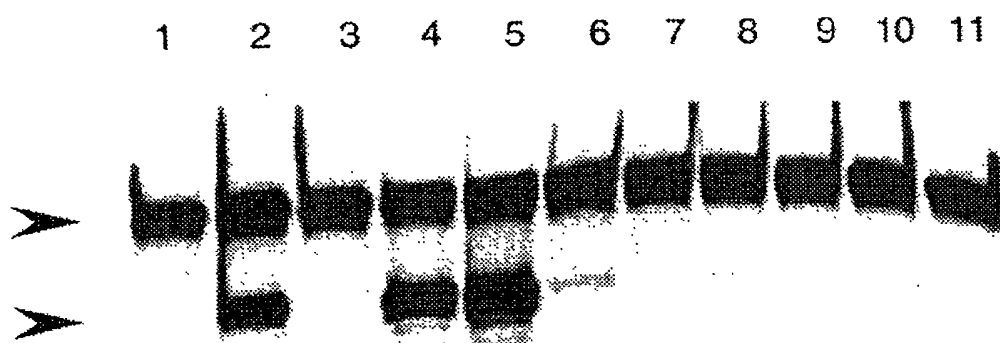
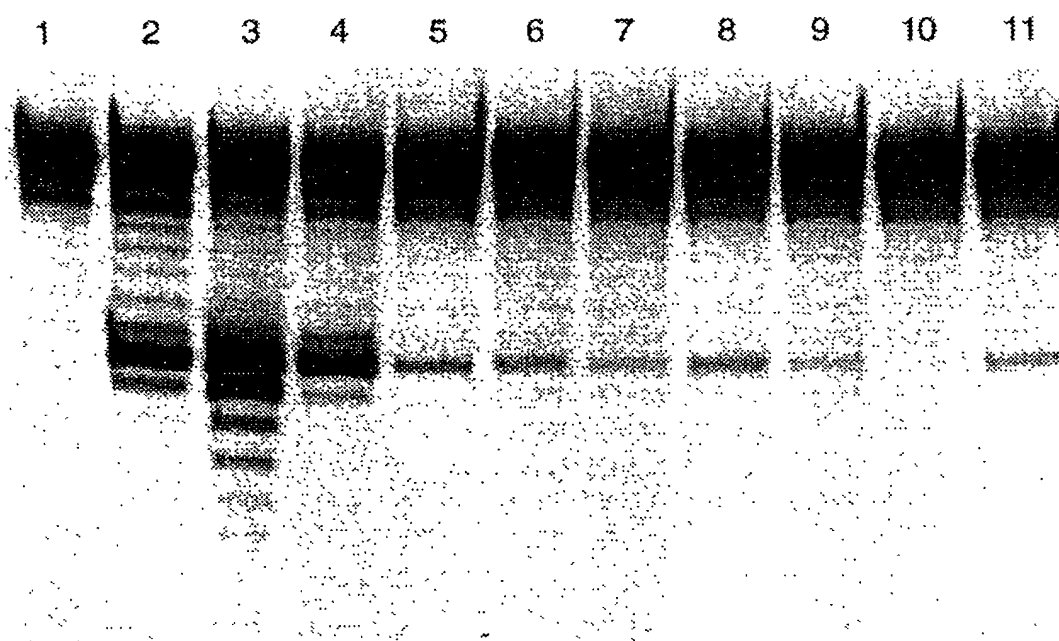
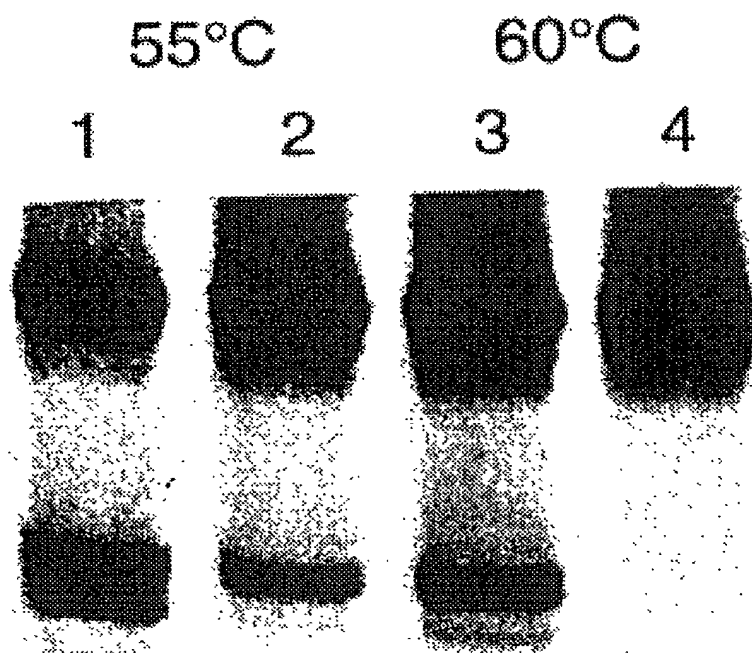
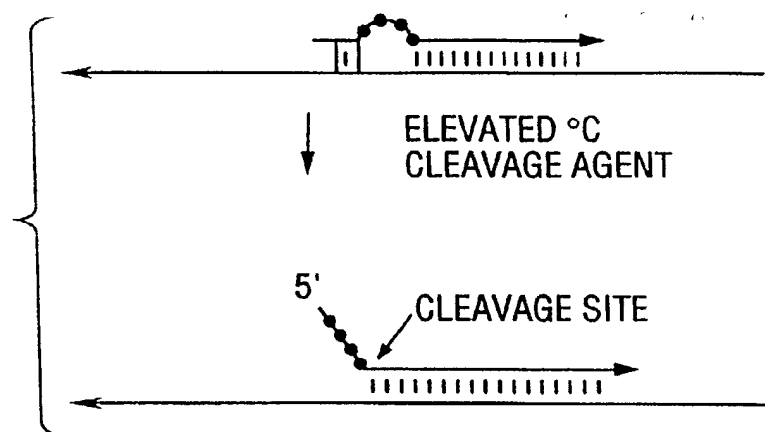
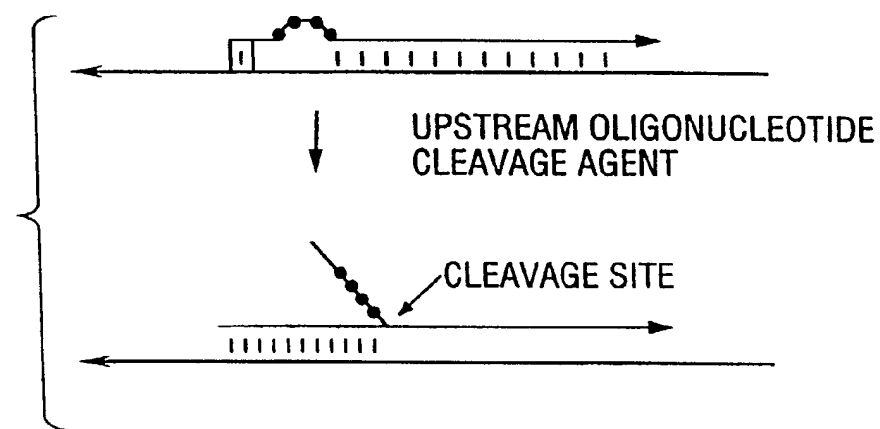


FIG. 37

**FIG. 38**



**FIG. 39**

**FIG. 40A****FIG. 40B**

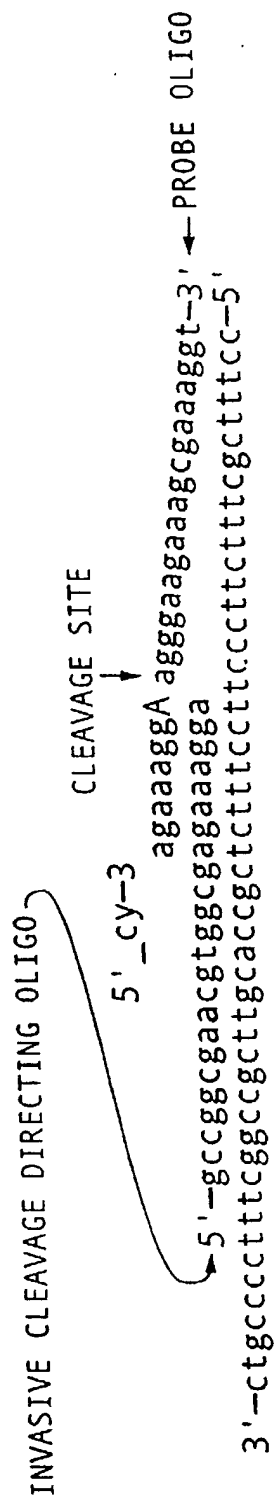
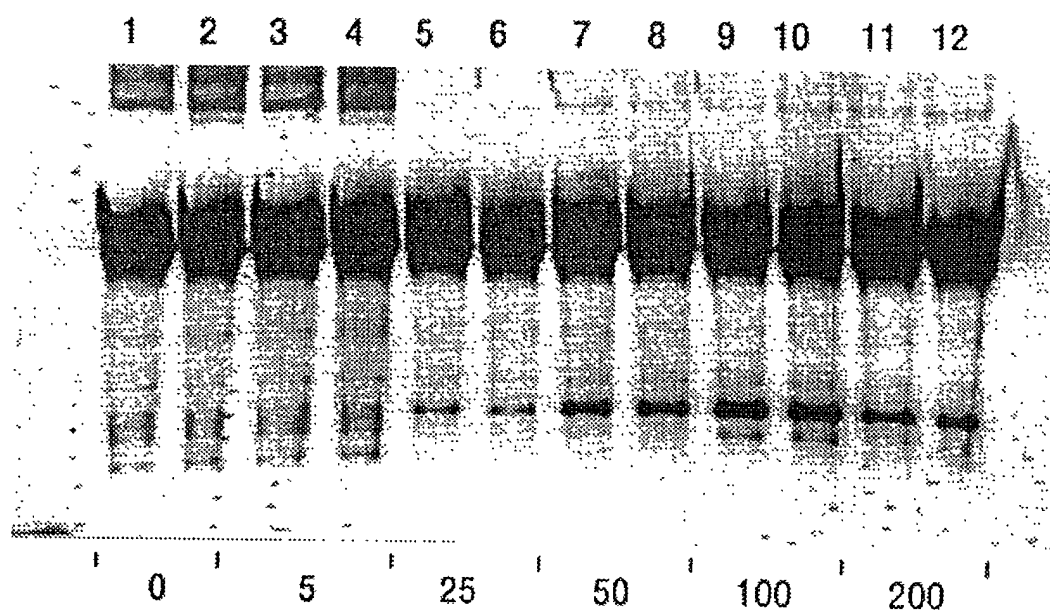
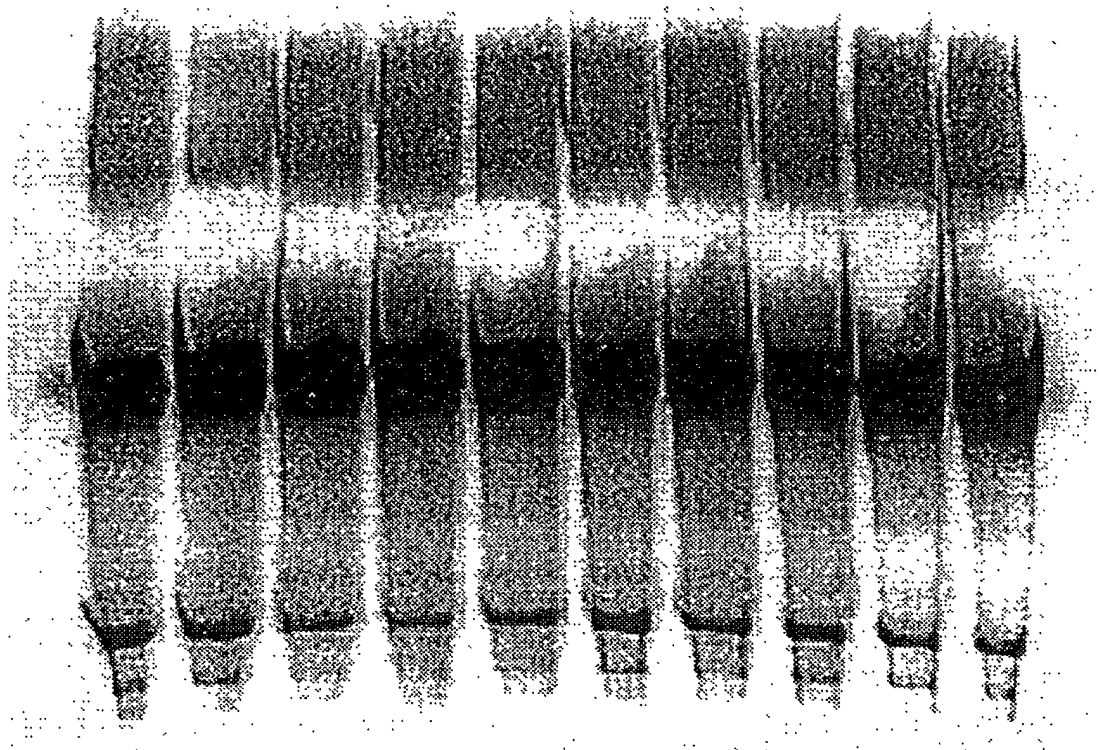


FIG. 41



**FIG. 42**

1 2 3 4 5 6 7 8 9 10



**FIG. 43**

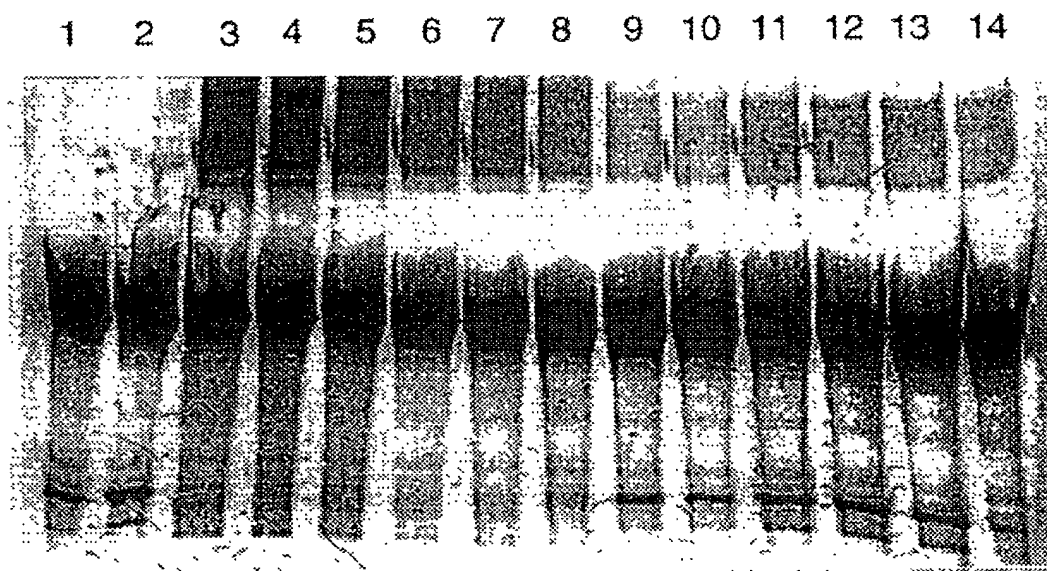


FIG. 44

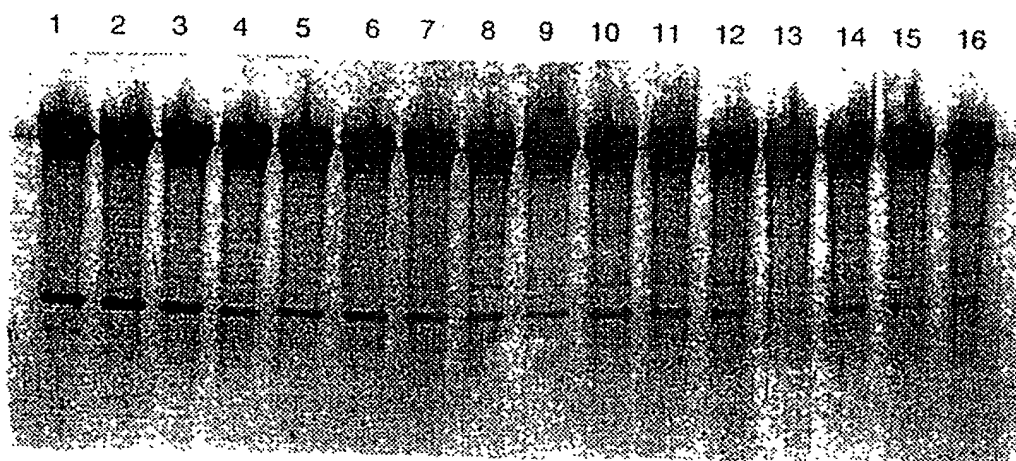


FIG. 45

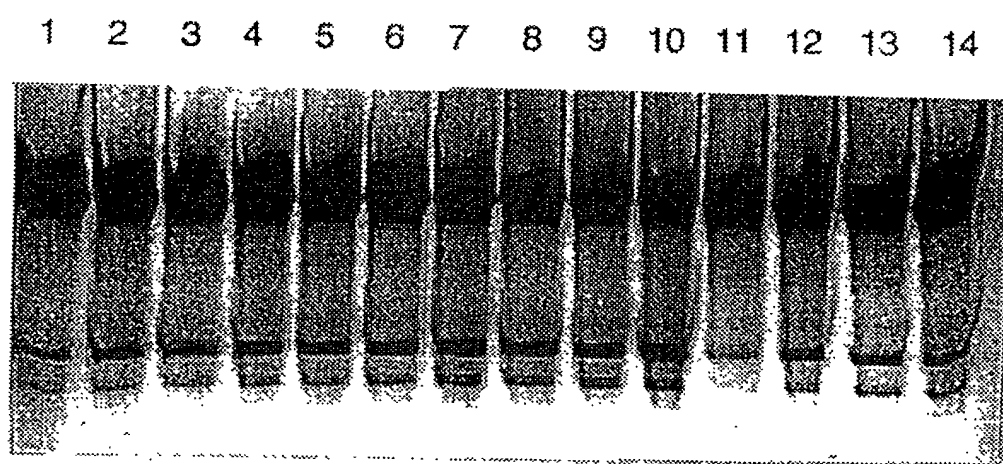


FIG. 46

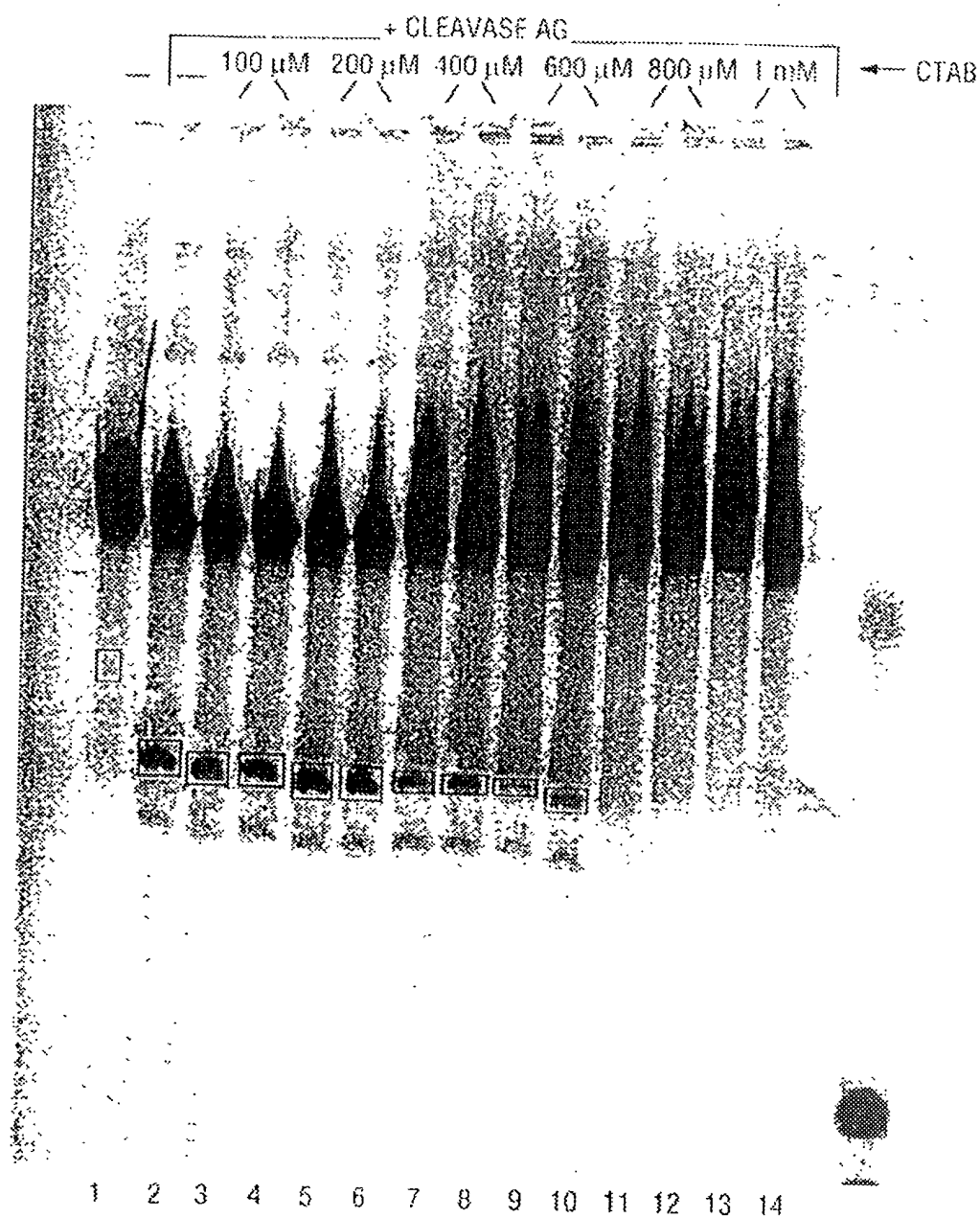


FIG. 47

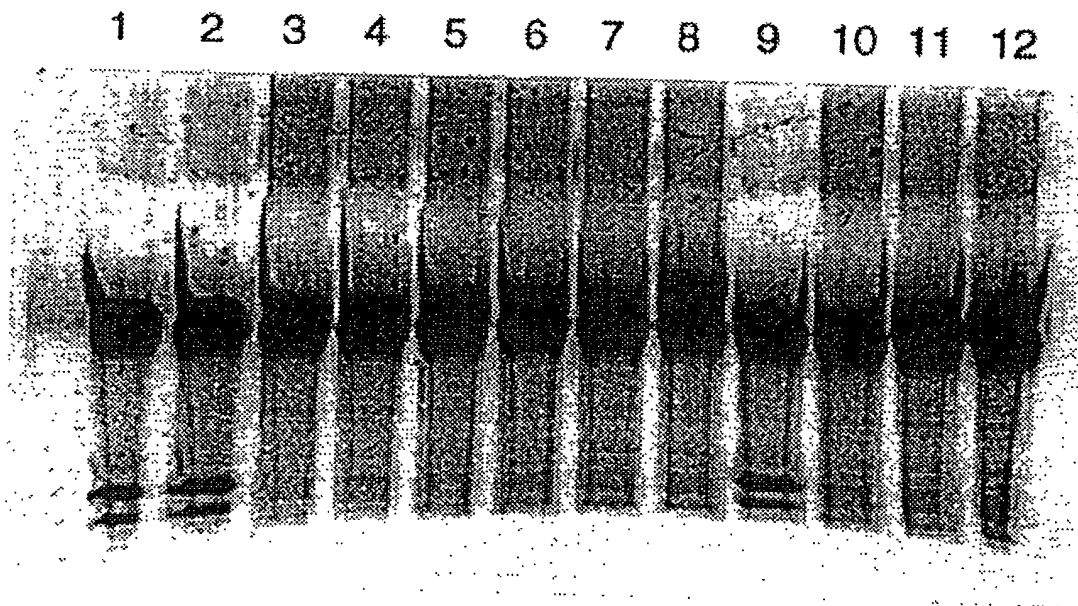
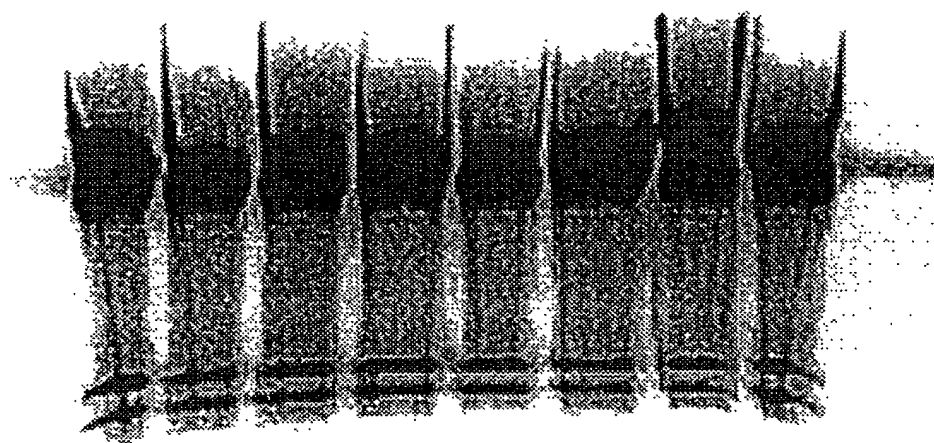


FIG. 48

1 2 3 4 5 6 7 8



**FIG. 49**



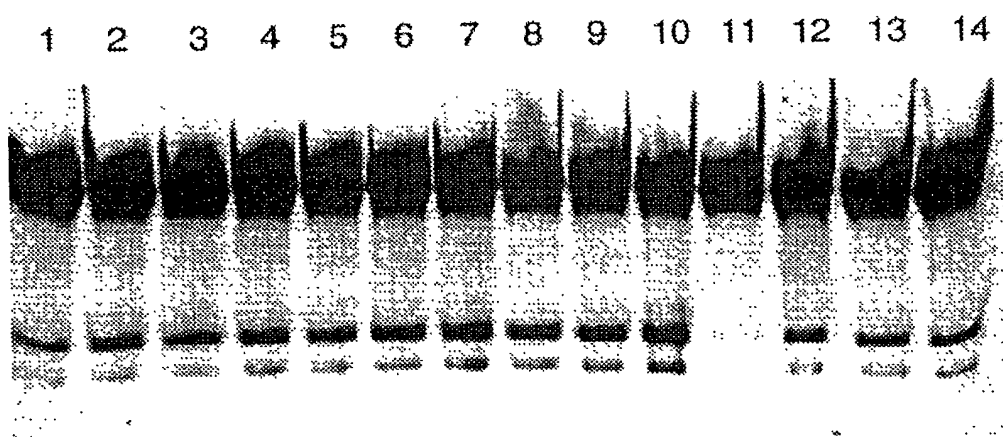
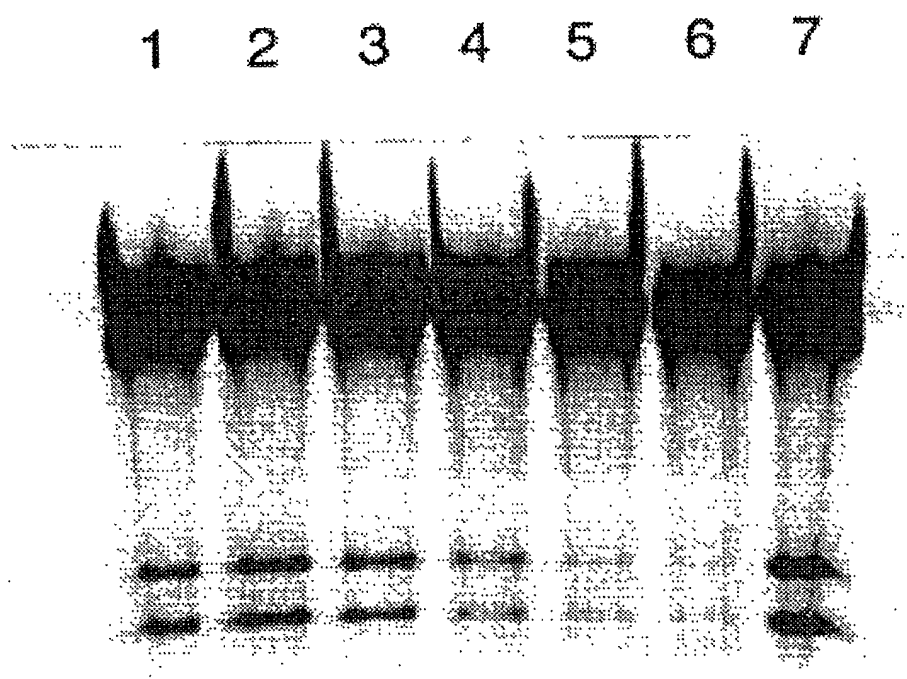


FIG. 50



**FIG. 51**

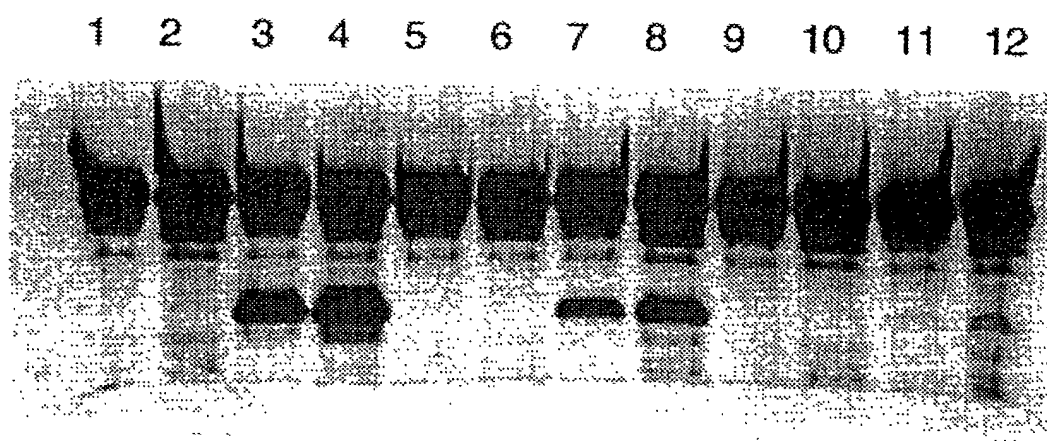
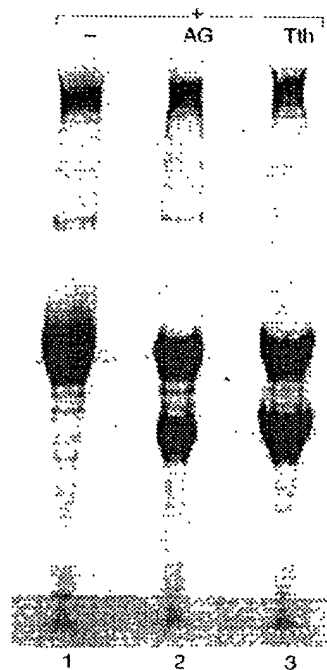
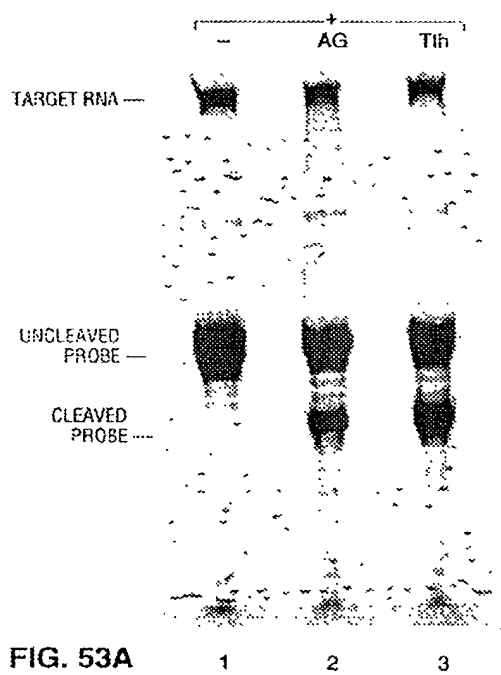


FIG. 52



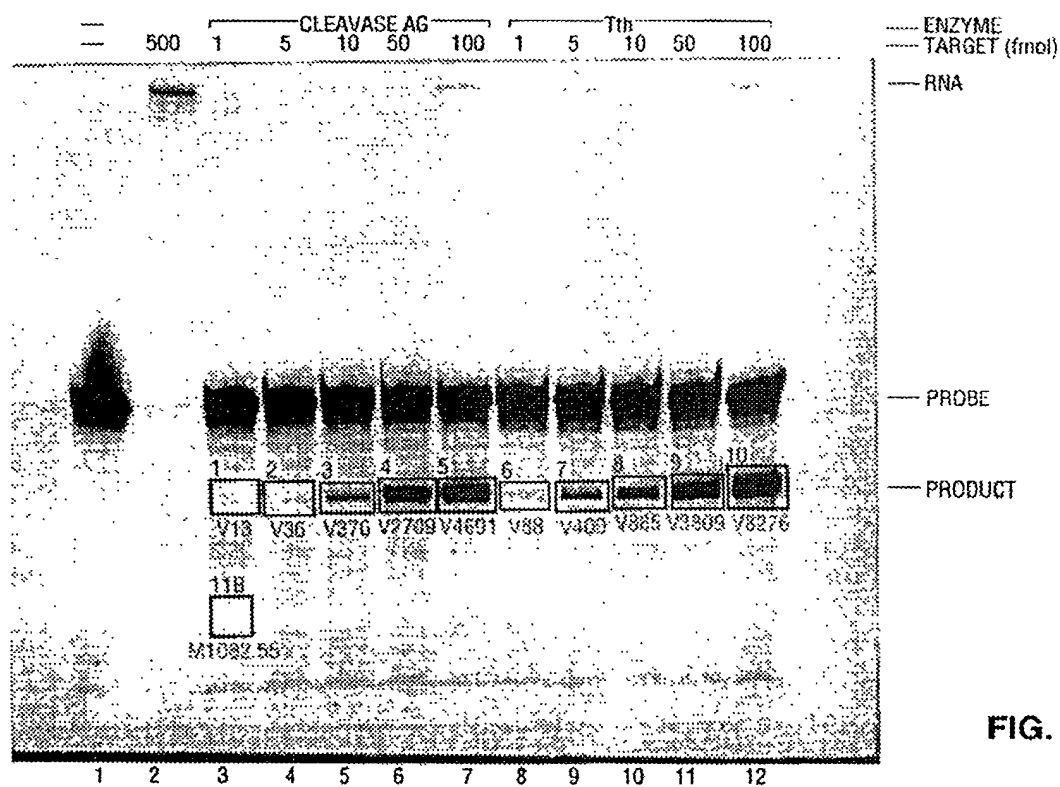
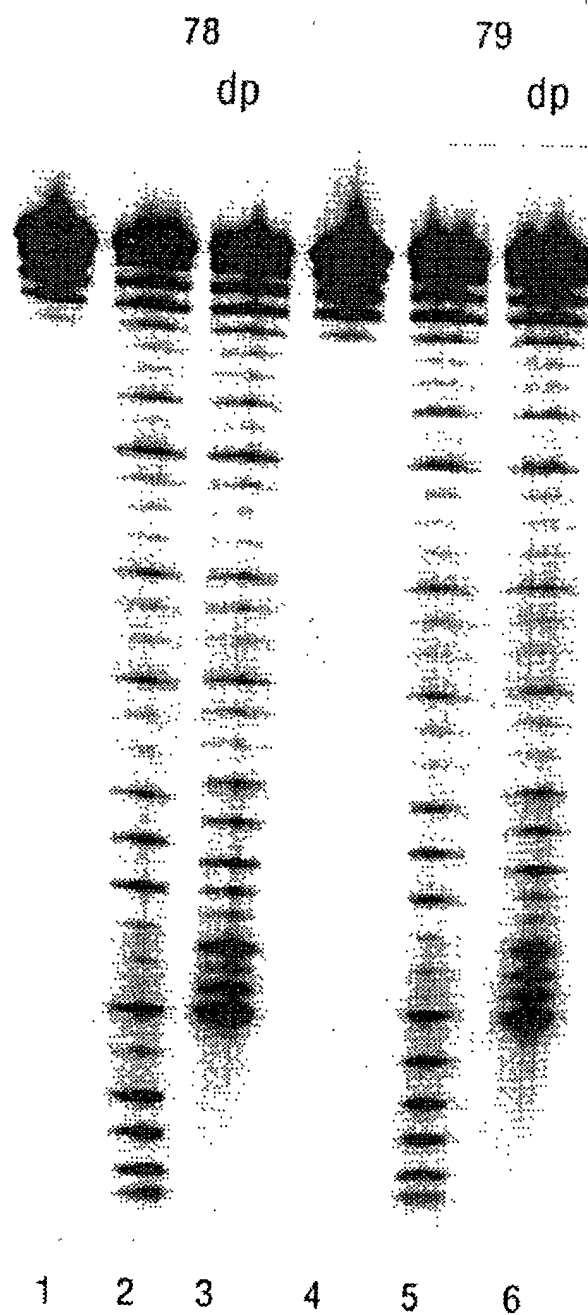


FIG. 54

**FIG. 55**

70 (C10 amino T's)  
74 (C6 amino T's)

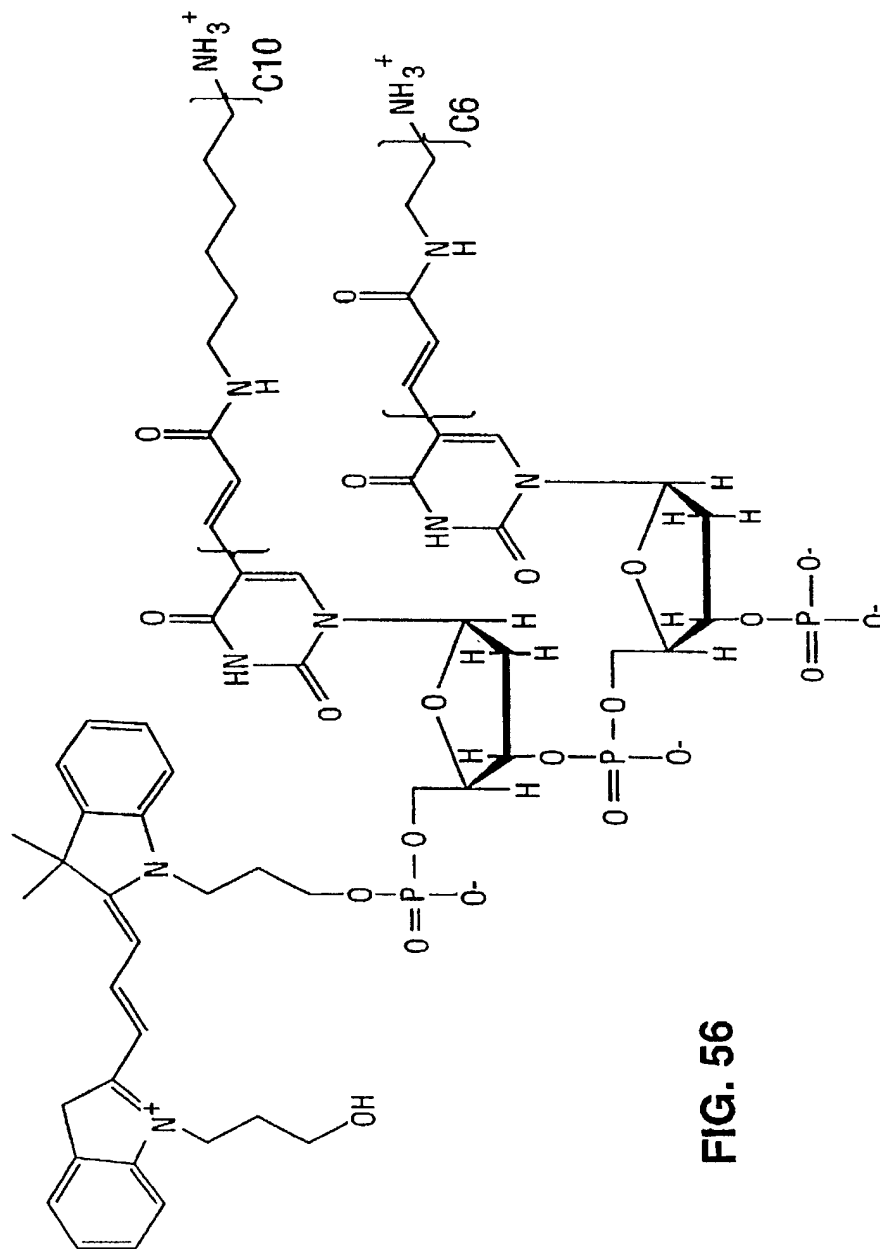


FIG. 56

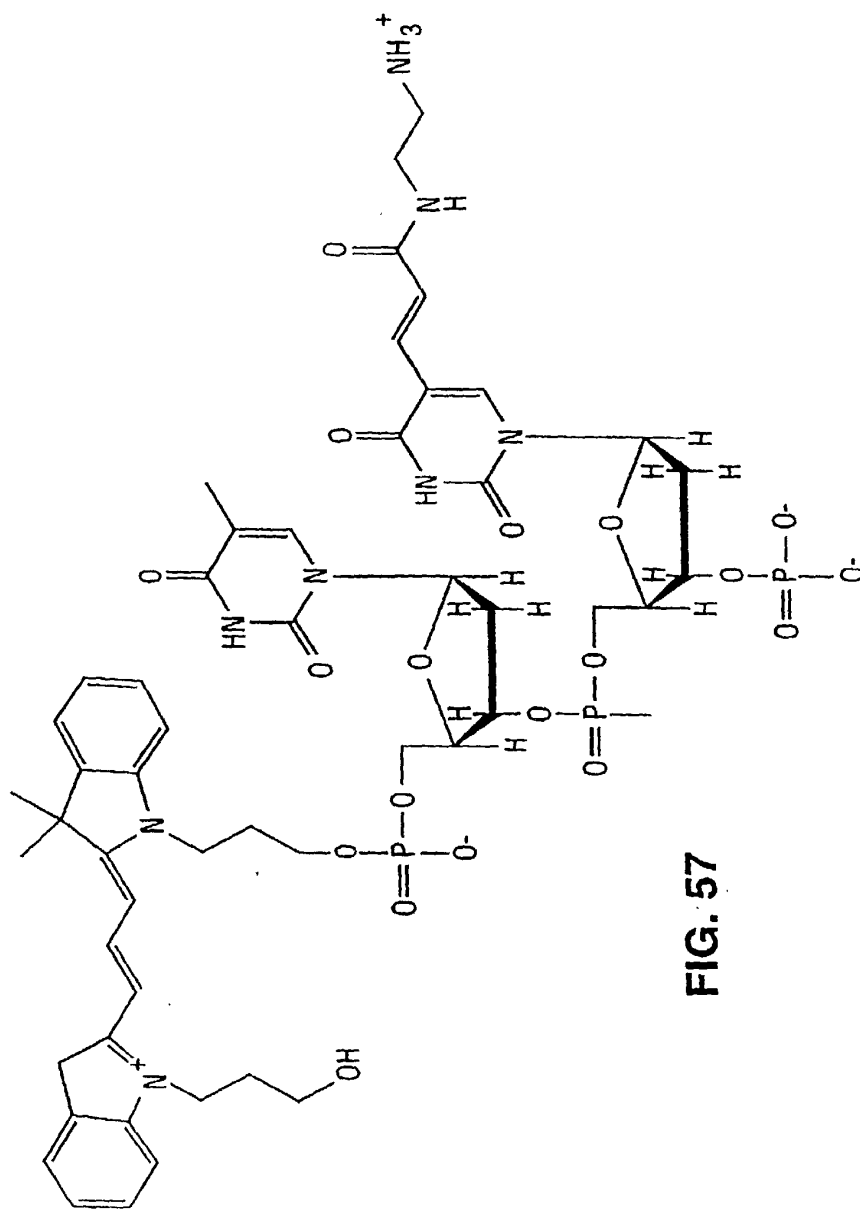


FIG. 57



76

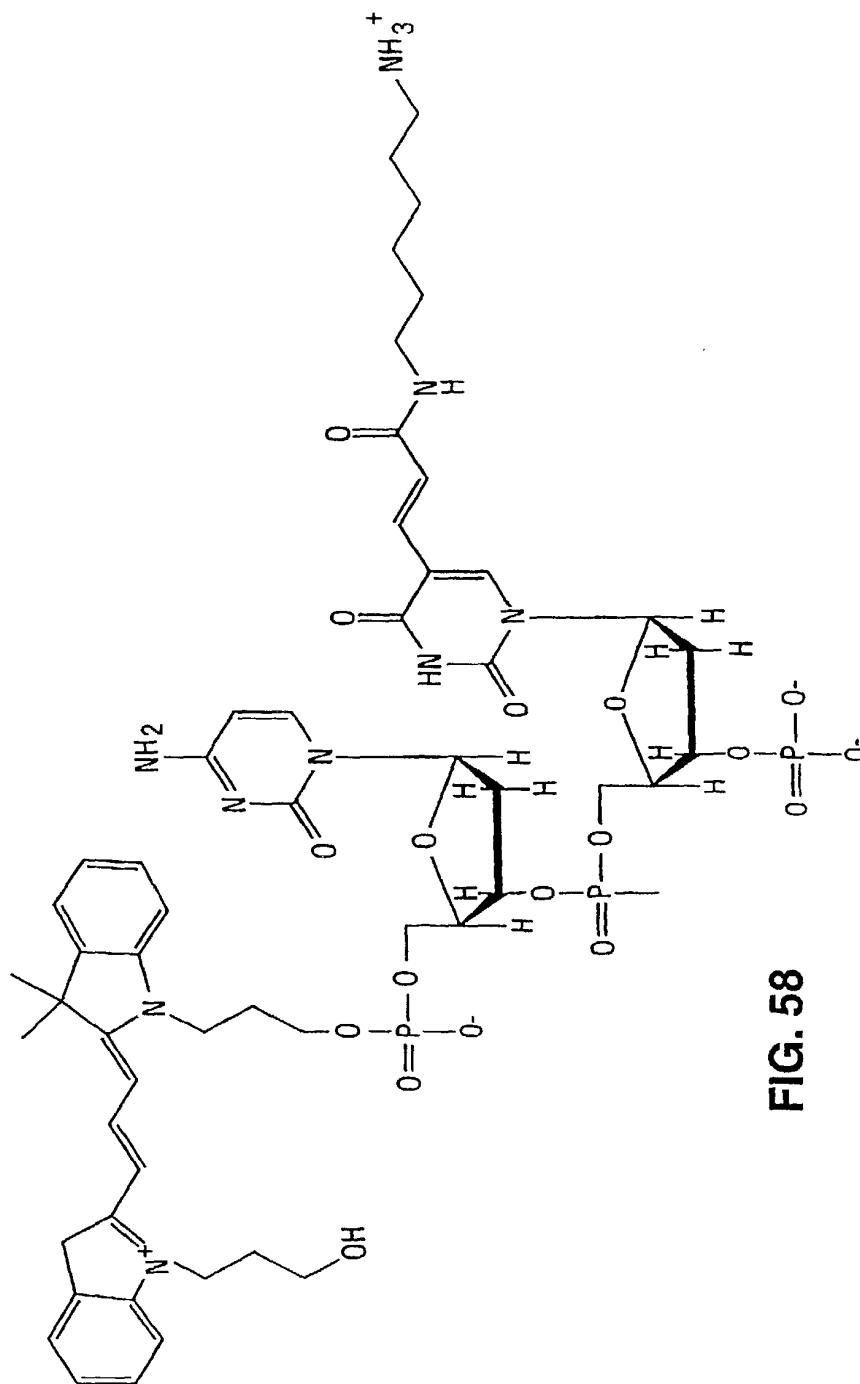
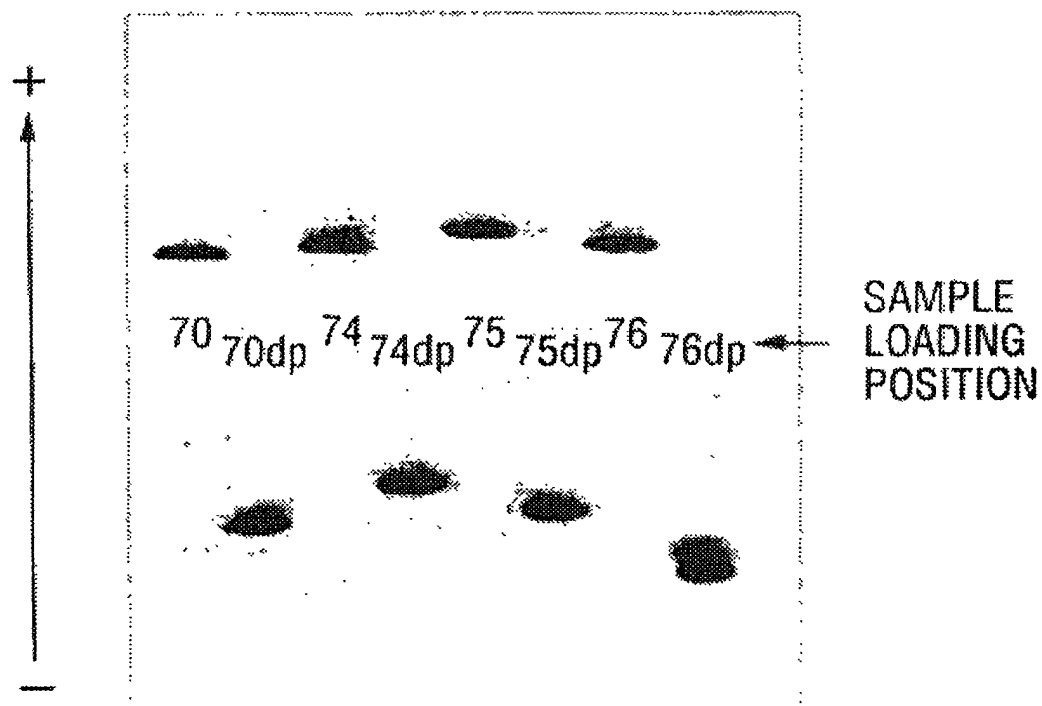


FIG. 58

**FIG. 59**

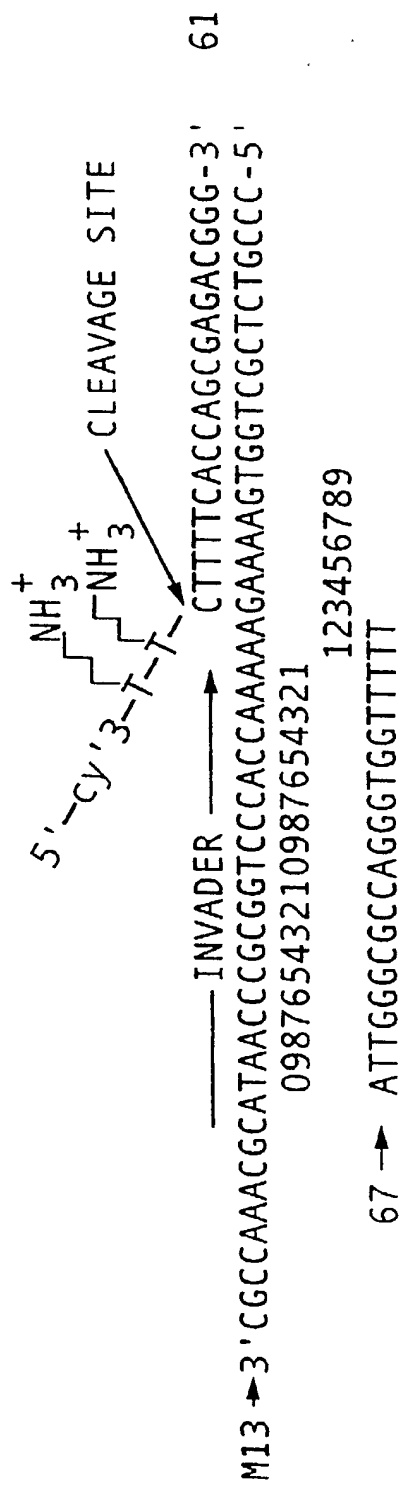


FIG. 60A

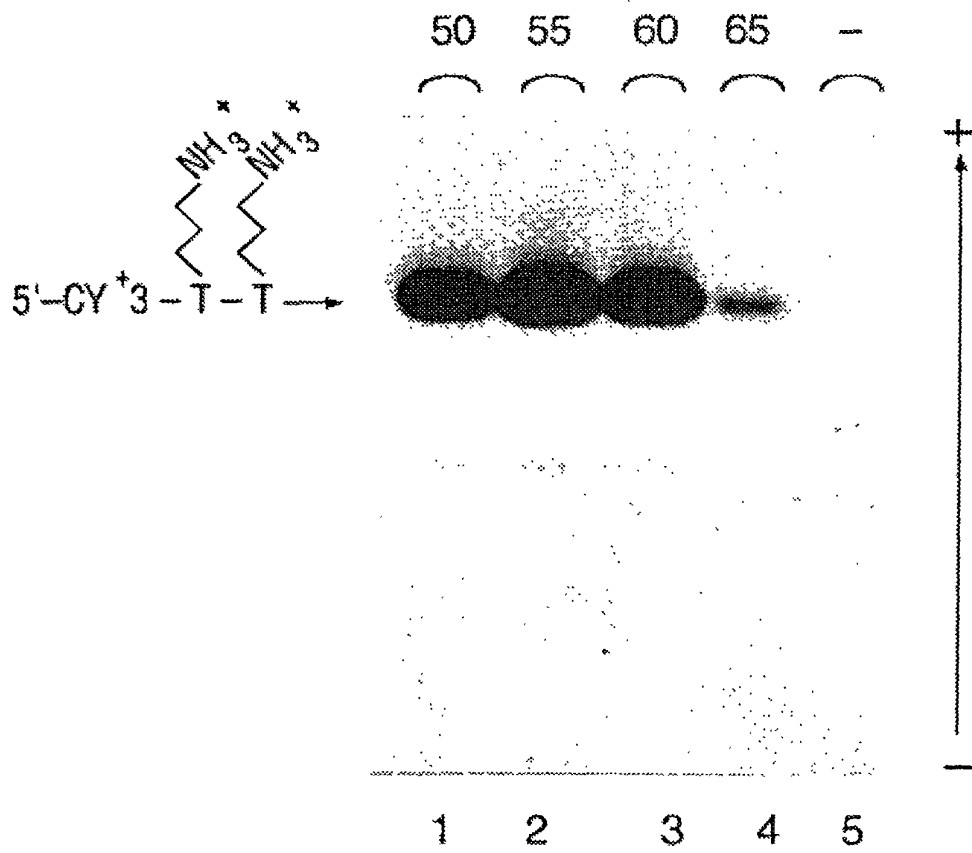


FIG. 60B

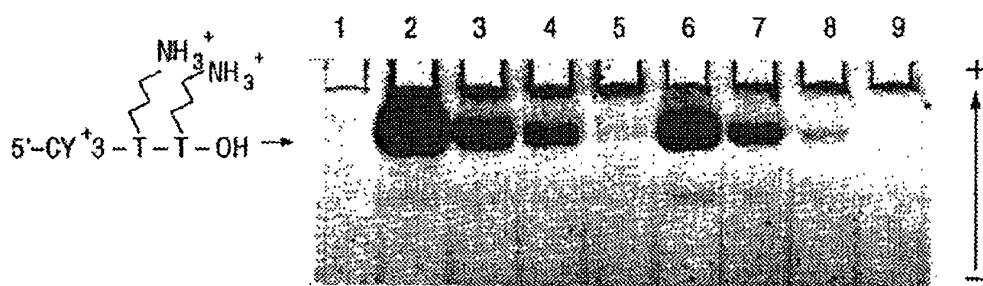


FIG. 61

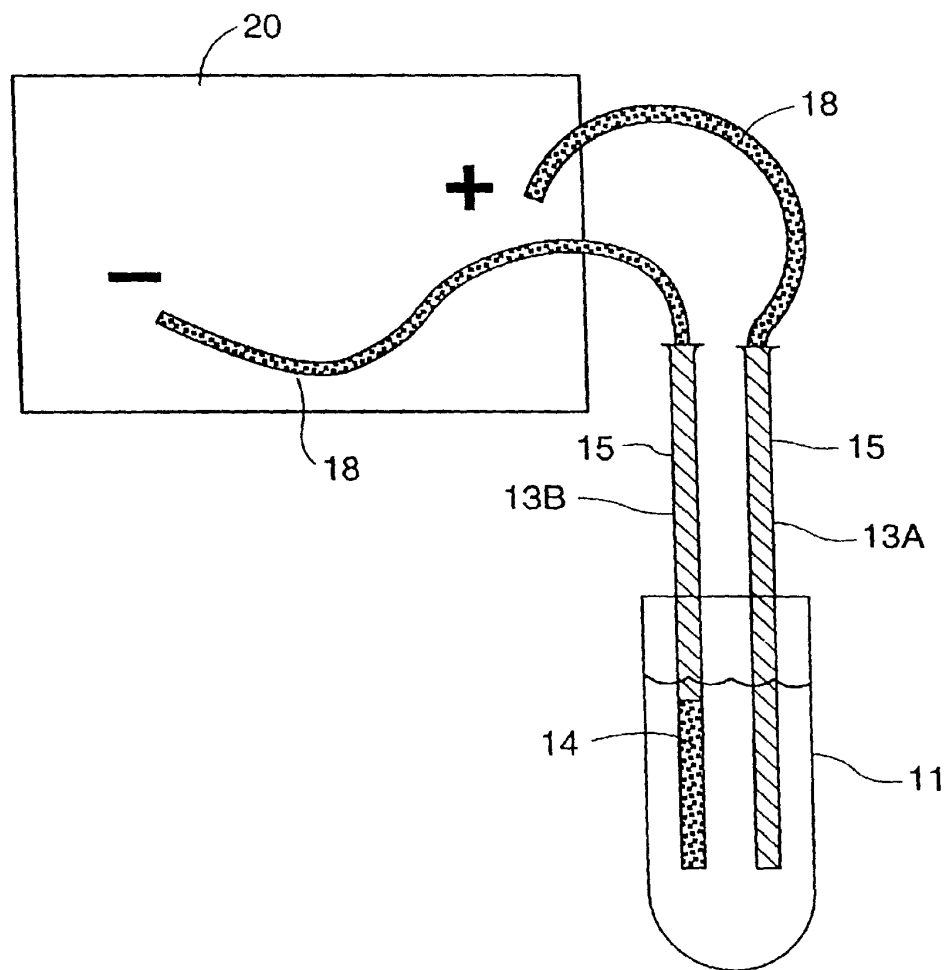


FIG. 62

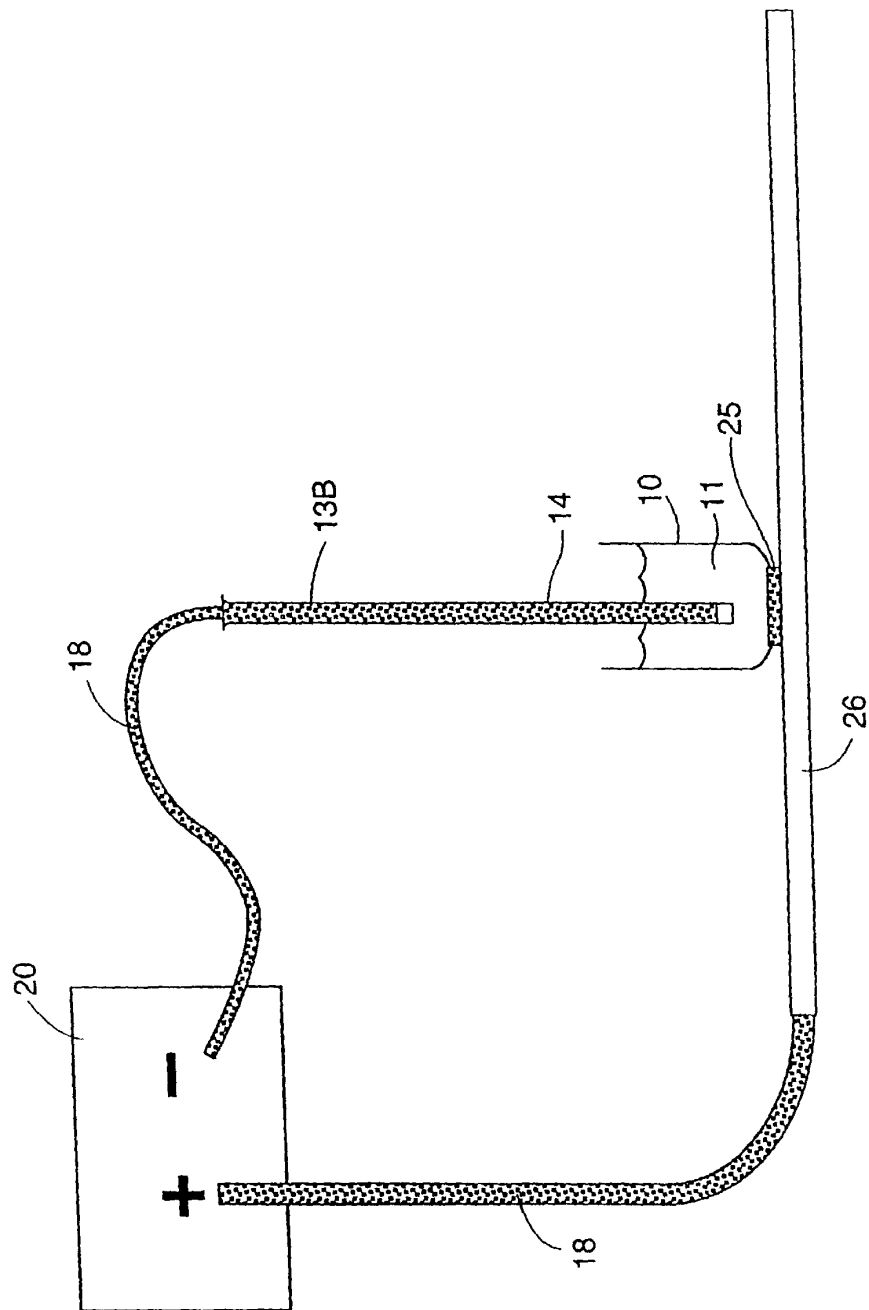


FIG. 63



FIG. 64





FIG. 65A



FIG. 65B



FIG. 65C



FIG. 65D

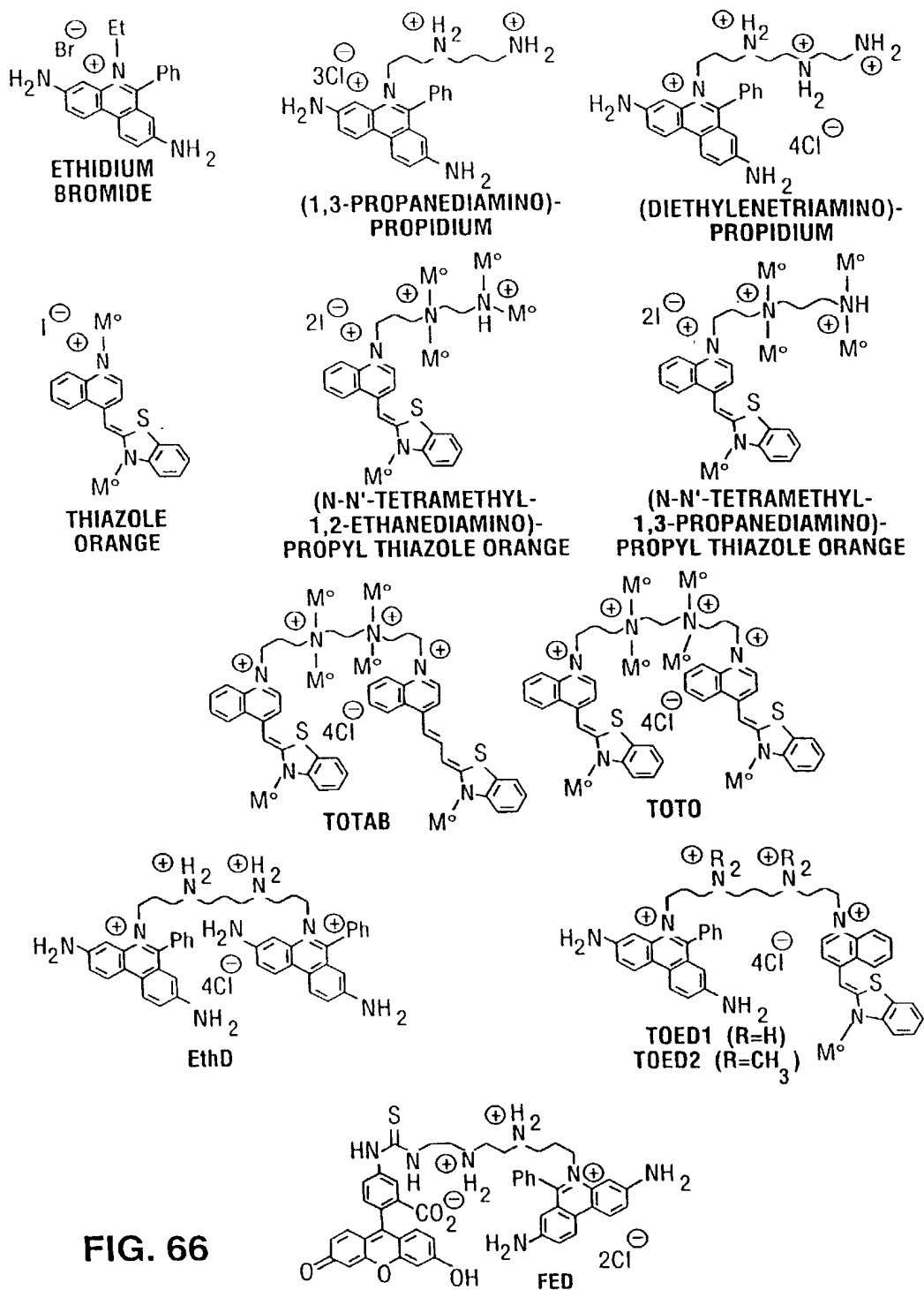


FIG. 66